

1/62

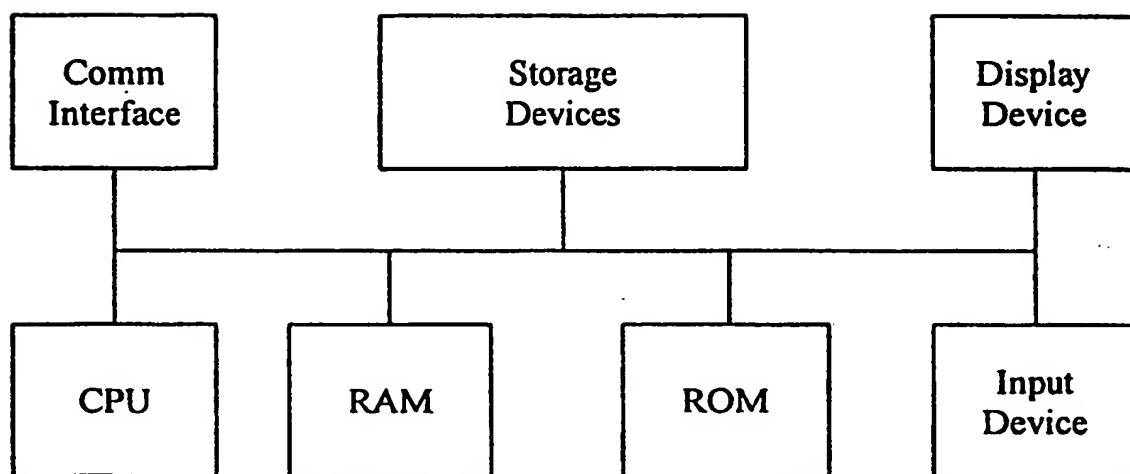


FIG. 1A

2/62

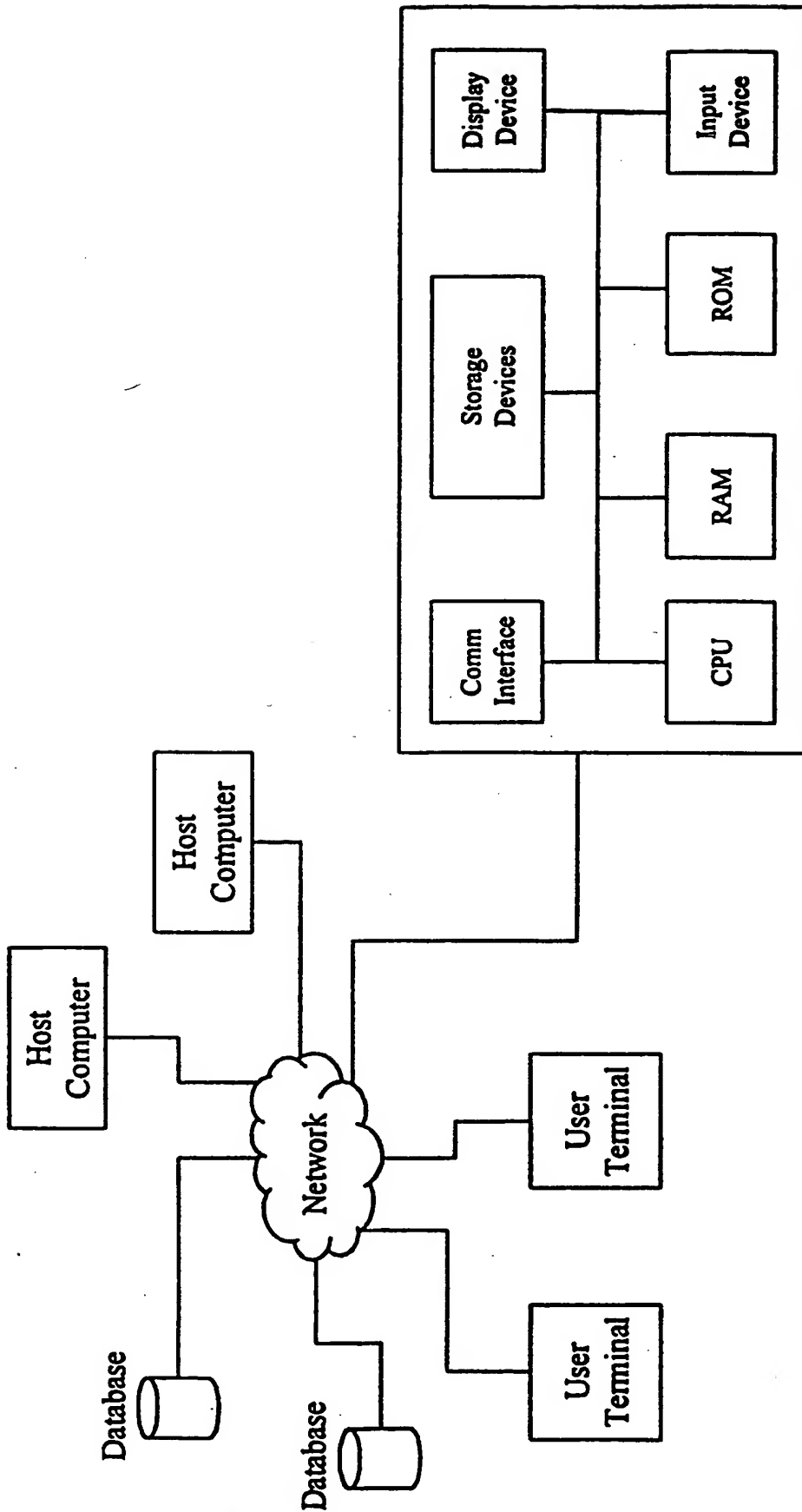
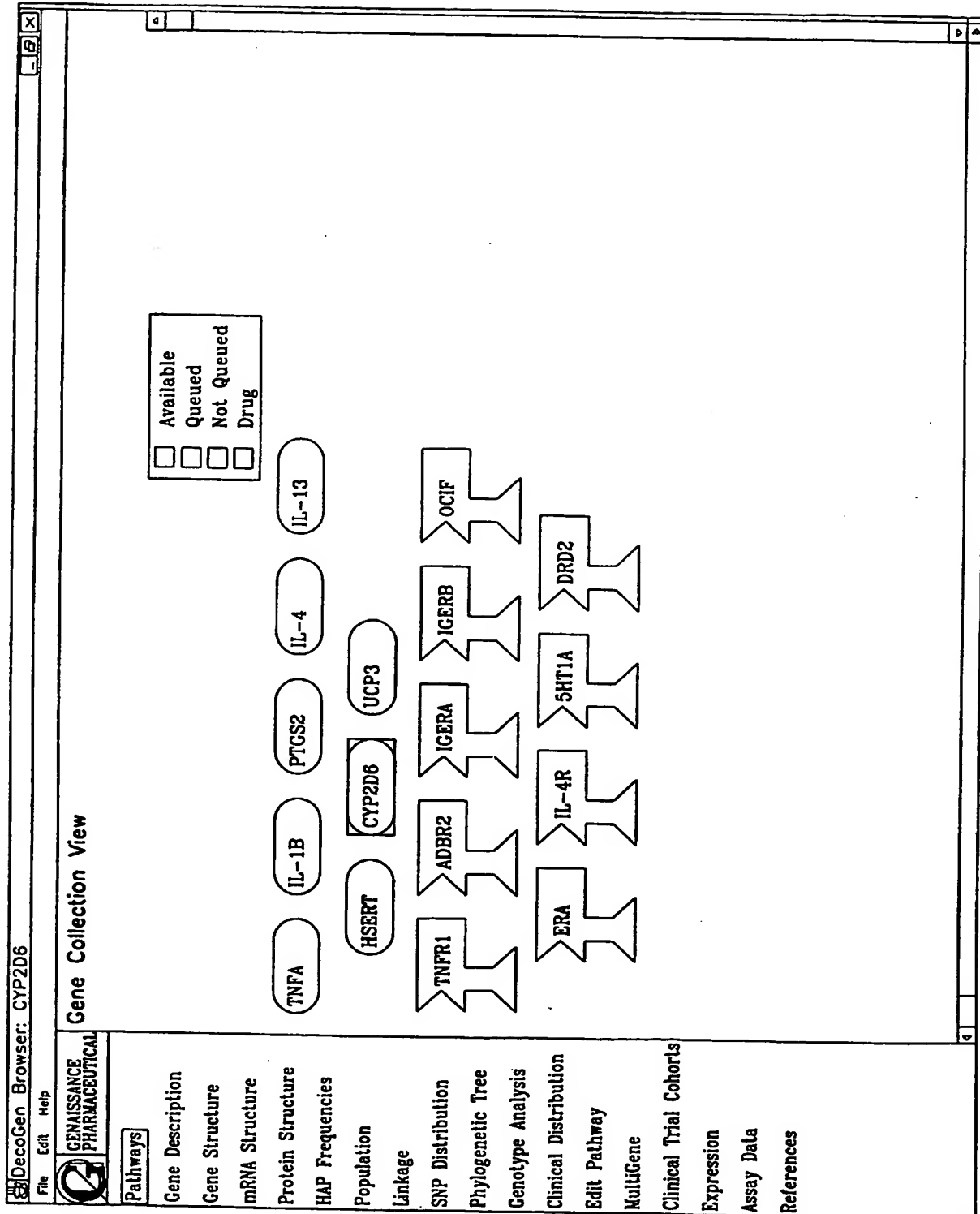


FIG. 1B

3/62

FIG. 2



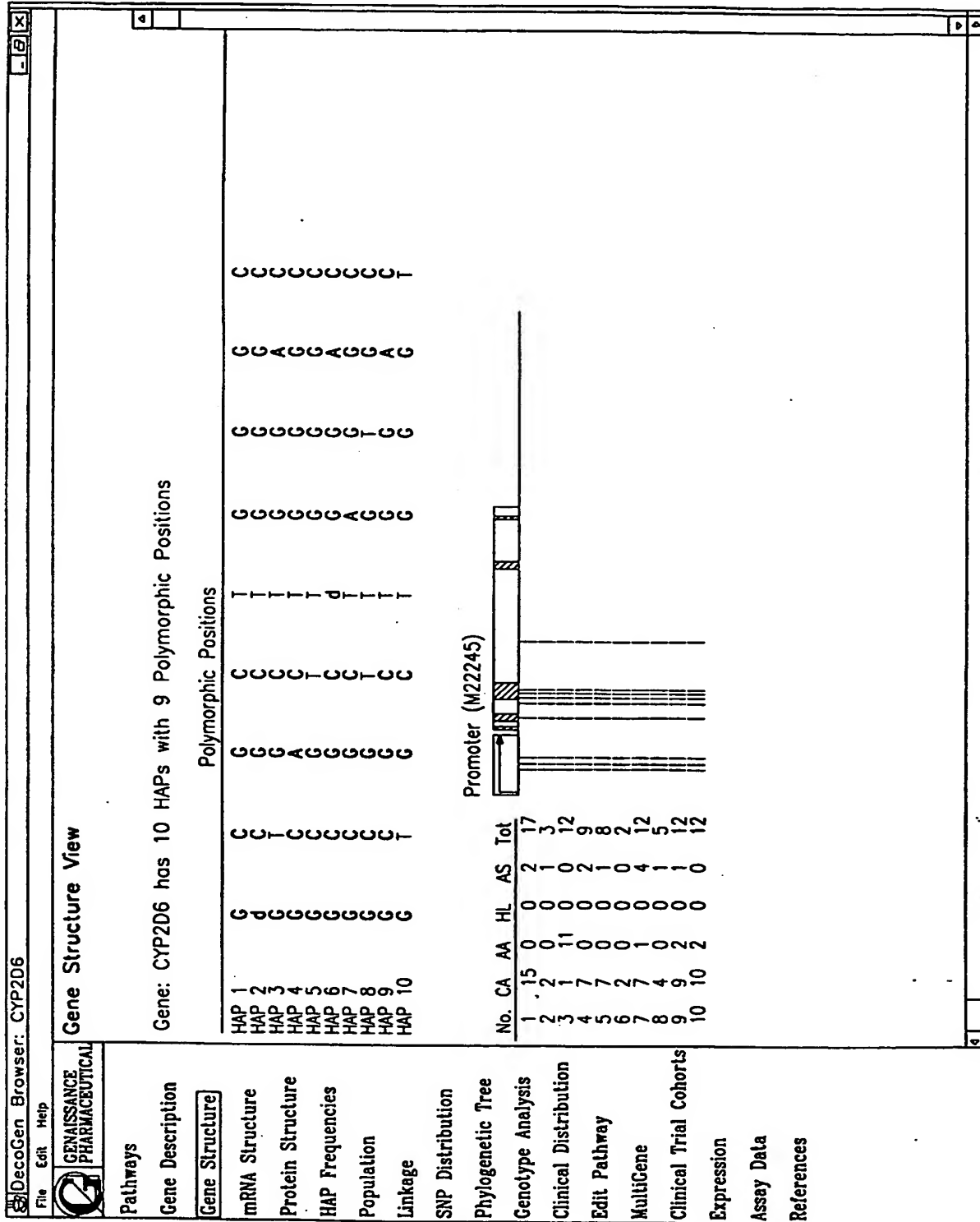
4/62

FIG. 3

| | | | | | | | | | | | | | | | | | | | | | |
|---------------------------------|--|------|--------|------------|--|----------|------------------|----------|--------------|--------|------|-------------|----|-----------------|----|----------------|----|---------------------------------|-------------------|---------------------------|-------------------|
| DecoGen Browser: CYP2D6 | | | | | | | | | | | | | | | | | | | | | |
| File Edit Help | | | | | | | | | | | | | | | | | | | | | |
| GENAISSANCE PHARMACEUTICAL | Gene Description View | | | | | | | | | | | | | | | | | | | | |
| Pathways | | | | | | | | | | | | | | | | | | | | | |
| Gene Description | | | | | | | | | | | | | | | | | | | | | |
| Gene Structure | | | | | | | | | | | | | | | | | | | | | |
| mRNA Structure | | | | | | | | | | | | | | | | | | | | | |
| Protein Structure | | | | | | | | | | | | | | | | | | | | | |
| HAP Frequencies | | | | | | | | | | | | | | | | | | | | | |
| Population | | | | | | | | | | | | | | | | | | | | | |
| Linkage | | | | | | | | | | | | | | | | | | | | | |
| SNP Distribution | | | | | | | | | | | | | | | | | | | | | |
| Phylogenetic Tree | | | | | | | | | | | | | | | | | | | | | |
| Genotype Analysis | | | | | | | | | | | | | | | | | | | | | |
| Clinical Distribution | | | | | | | | | | | | | | | | | | | | | |
| Edit Pathway | | | | | | | | | | | | | | | | | | | | | |
| MultiGene | | | | | | | | | | | | | | | | | | | | | |
| Clinical Trial Cohorts | | | | | | | | | | | | | | | | | | | | | |
| Expression | | | | | | | | | | | | | | | | | | | | | |
| Assay Data | | | | | | | | | | | | | | | | | | | | | |
| References | | | | | | | | | | | | | | | | | | | | | |
| | <table> <tr> <td>Name</td><td>CYP2D6</td></tr> <tr> <td>Definition</td><td>Human cytochrome P450 IID6 (CYP2D6) gene</td></tr> <tr> <td>Function</td><td>Metabolic enzyme</td></tr> <tr> <td>Organism</td><td>Homo Sapiens</td></tr> <tr> <td>Length</td><td>9432</td></tr> <tr> <td>No Features</td><td>13</td></tr> <tr> <td>Population Size</td><td>46</td></tr> <tr> <td>No. Haplotypes</td><td>10</td></tr> <tr> <td>Nucleotide Polymorphism (theta)</td><td>5.6E-4 +/- 3.1E-4</td></tr> <tr> <td>Nucleotide Diversity (pi)</td><td>2.8E-4 +/- 1.8E-4</td></tr> </table> | Name | CYP2D6 | Definition | Human cytochrome P450 IID6 (CYP2D6) gene | Function | Metabolic enzyme | Organism | Homo Sapiens | Length | 9432 | No Features | 13 | Population Size | 46 | No. Haplotypes | 10 | Nucleotide Polymorphism (theta) | 5.6E-4 +/- 3.1E-4 | Nucleotide Diversity (pi) | 2.8E-4 +/- 1.8E-4 |
| Name | CYP2D6 | | | | | | | | | | | | | | | | | | | | |
| Definition | Human cytochrome P450 IID6 (CYP2D6) gene | | | | | | | | | | | | | | | | | | | | |
| Function | Metabolic enzyme | | | | | | | | | | | | | | | | | | | | |
| Organism | Homo Sapiens | | | | | | | | | | | | | | | | | | | | |
| Length | 9432 | | | | | | | | | | | | | | | | | | | | |
| No Features | 13 | | | | | | | | | | | | | | | | | | | | |
| Population Size | 46 | | | | | | | | | | | | | | | | | | | | |
| No. Haplotypes | 10 | | | | | | | | | | | | | | | | | | | | |
| Nucleotide Polymorphism (theta) | 5.6E-4 +/- 3.1E-4 | | | | | | | | | | | | | | | | | | | | |
| Nucleotide Diversity (pi) | 2.8E-4 +/- 1.8E-4 | | | | | | | | | | | | | | | | | | | | |

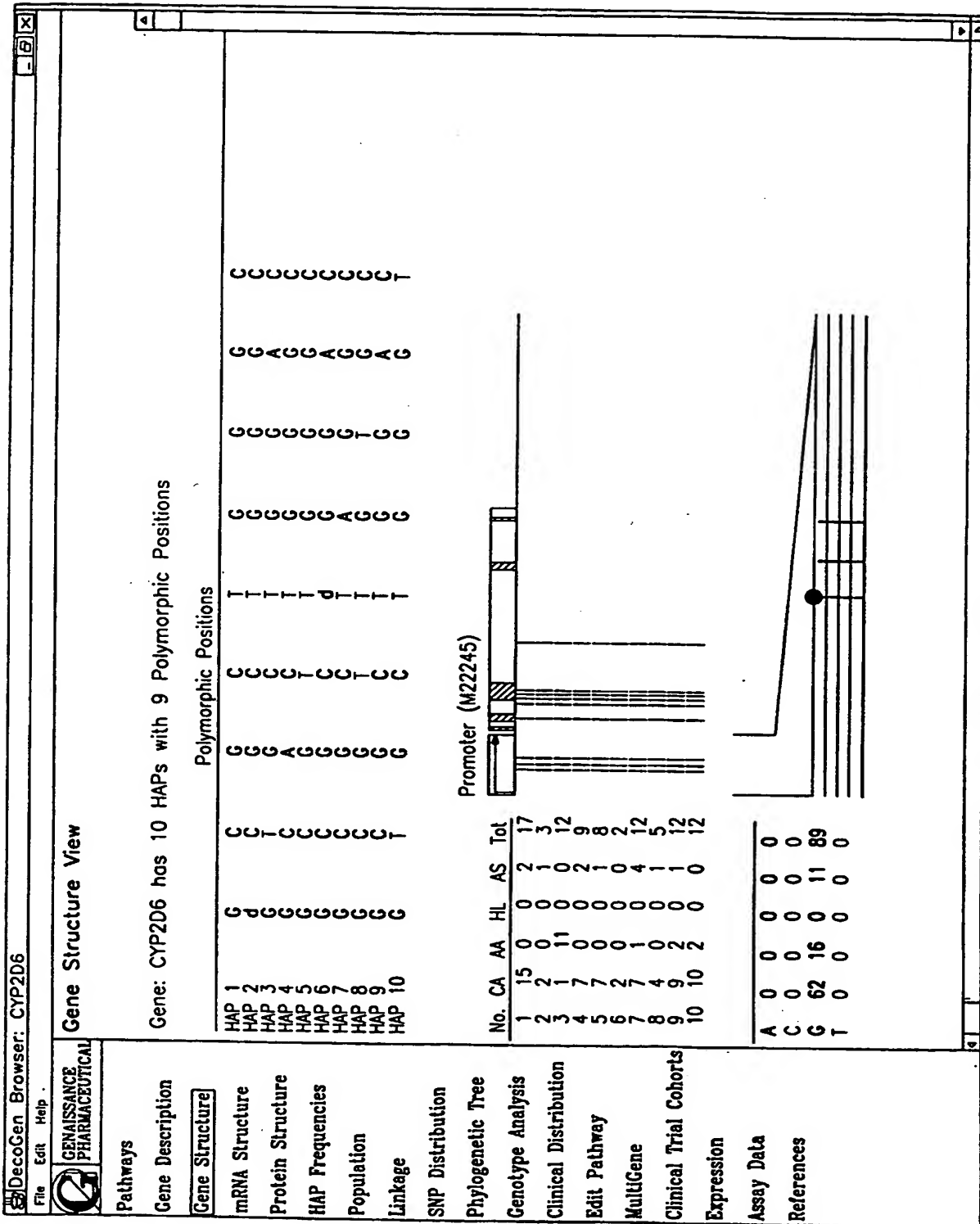
5/62

FIG. 4a

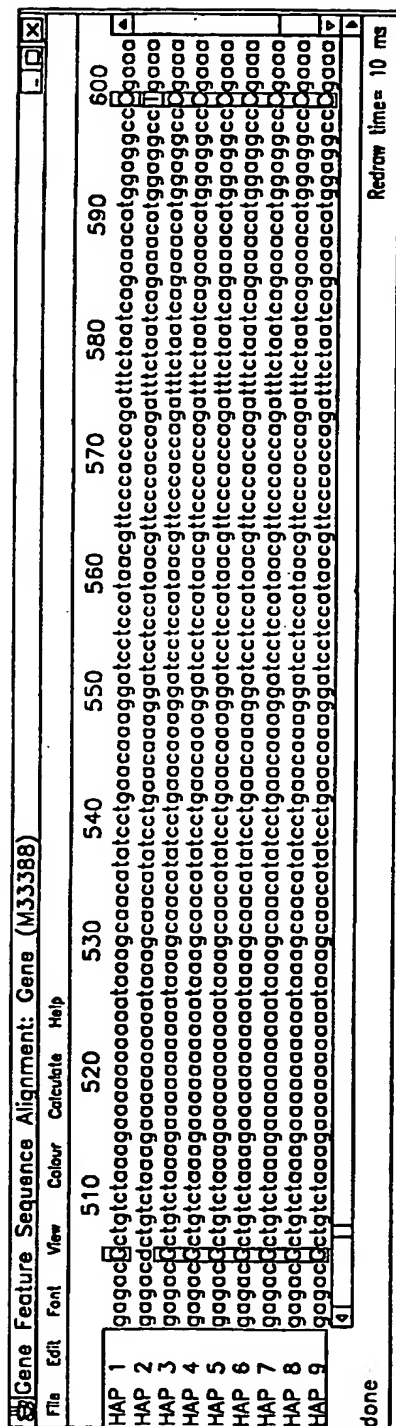


6/62

FIG. 4b



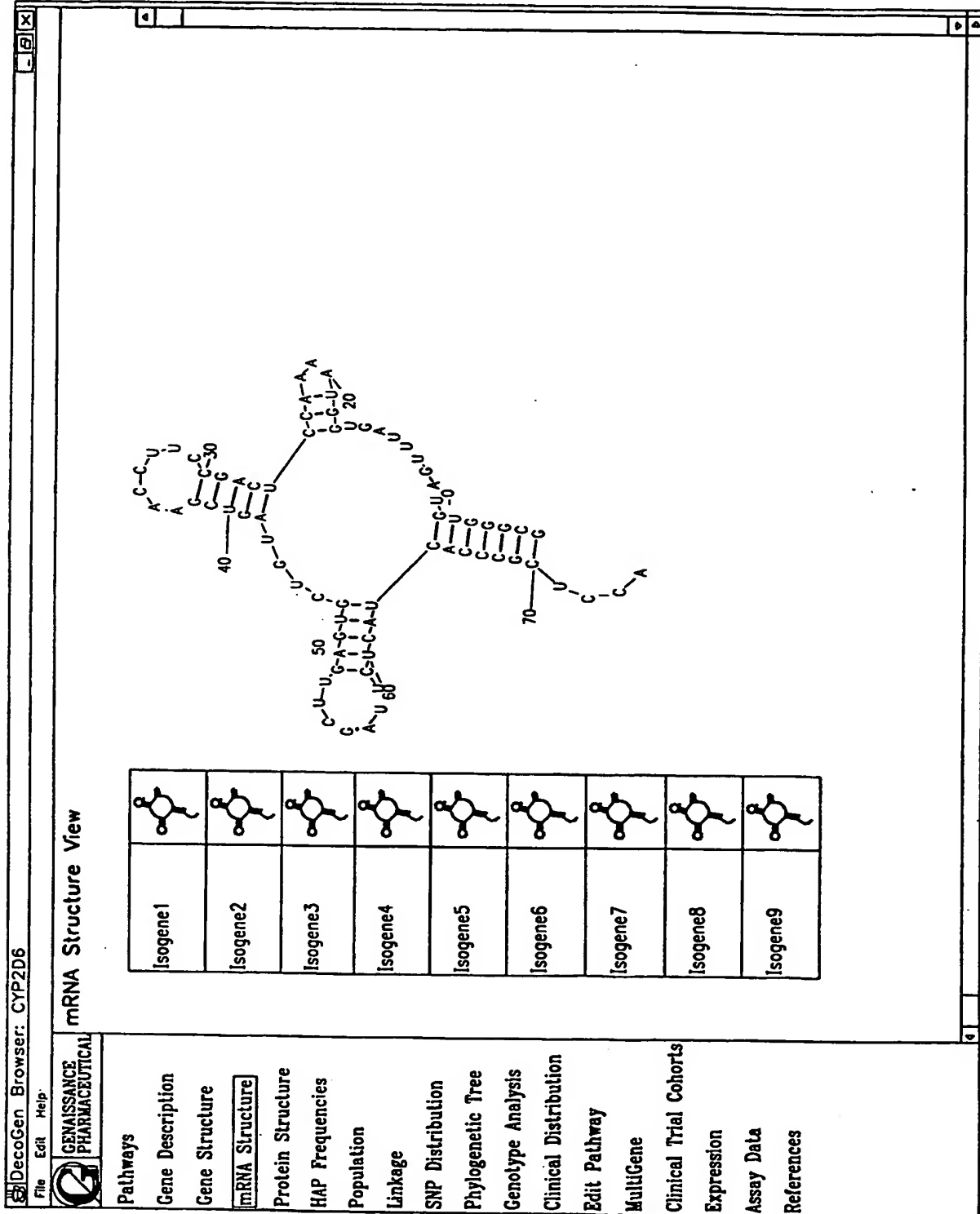
7/62



56

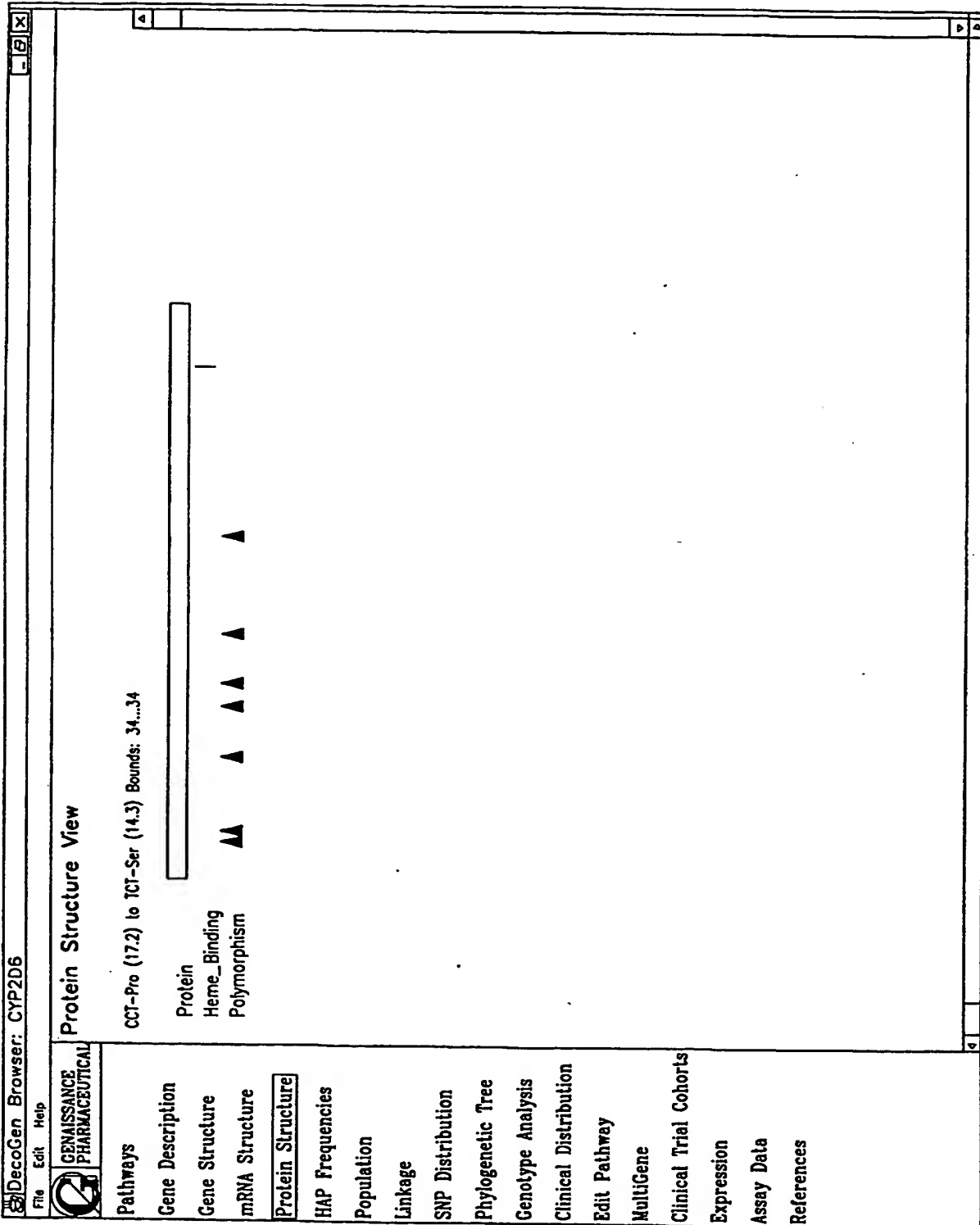
8/62

FIG. 6



9/62

FIG. 7

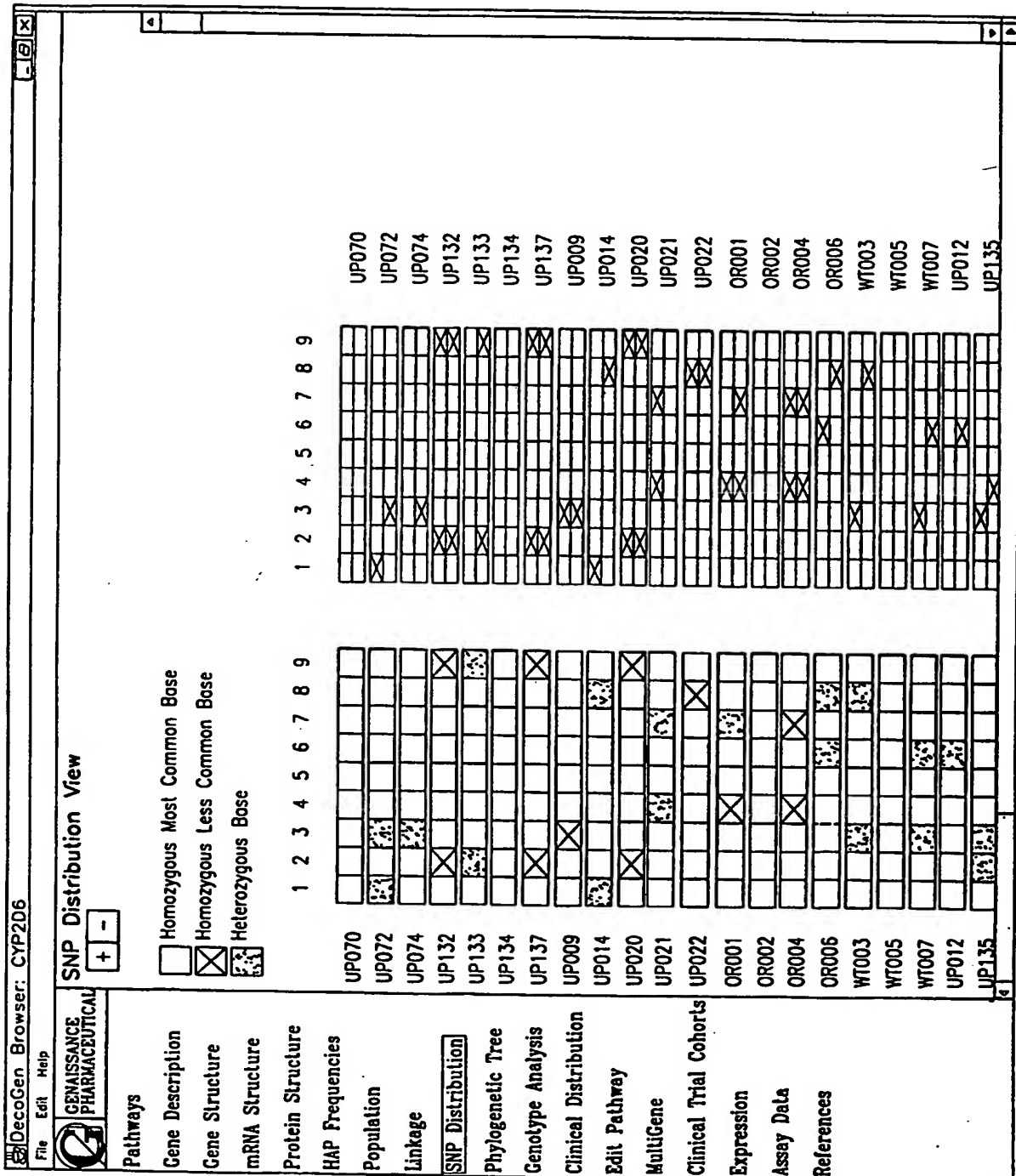


10/62

FIG. 8

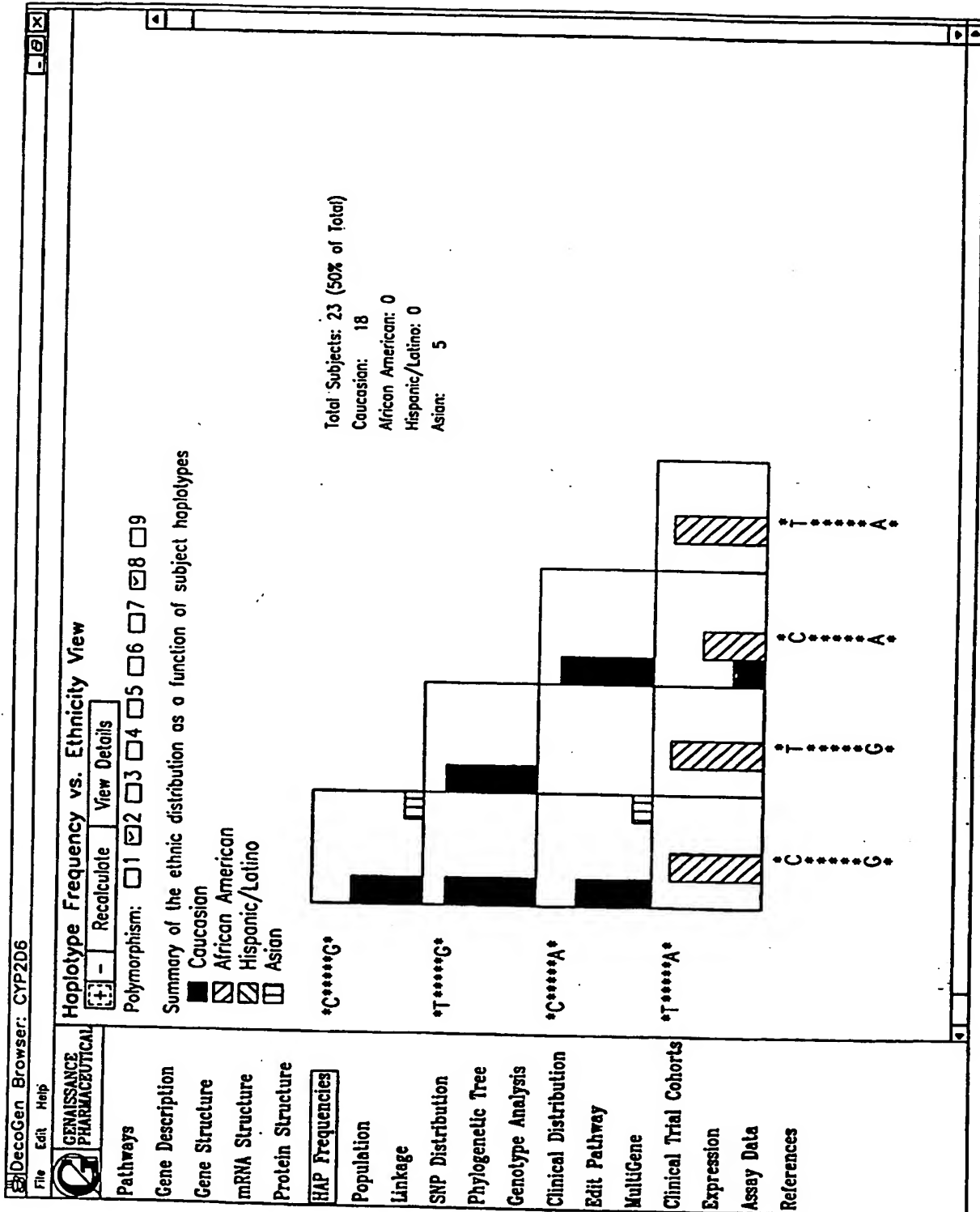
| | | | | | | | | | |
|----------------------------|-------|-----------|-----|--------|-----------|----------|------|--|--|
| DecoGen Browser: CYP2D6 | | | | | | | | | |
| File Edit Help | | | | | | | | | |
| GENAissance PHARMACEUTICAL | | | | | | | | | |
| Population View | | | | | | | | | |
| Pathways | PID | Ethnicity | Age | Gender | HAP 1 | HAP 2 | Test | | |
| Gene Description | UP070 | CA | 99 | F | GGCTGGGC | GGCTGGGC | 0.1 | | |
| Gene Structure | UP072 | CA | 99 | F | dCCCTGGGC | GCCTGGGC | 0.2 | | |
| mRNA Structure | UP074 | CA | 99 | F | GGCTGGGC | GCCTGGGC | 0.2 | | |
| Protein Structure | UP132 | CA | 99 | M | GTCTGGGT | GTCTGGGT | 0.3 | | |
| HAP Frequencies | UP133 | CA | 99 | M | GGCTGGGC | GTCTGGGT | 0.2 | | |
| Population | UP134 | CA | 99 | F | GGCTGGGC | GGCTGGGC | 0.1 | | |
| Linkage | UP137 | CA | 99 | M | GTCTGGGT | GTCTGGGT | 0.1 | | |
| SNP Distribution | UP009 | CA | 99 | F | GCCTGGGC | GCCTGGGC | 0.1 | | |
| Phylogenetic Tree | UP014 | CA | 99 | F | dCCCTGGGC | GGCTGGAC | 0.3 | | |
| Genotype Analysis | UP020 | CA | 99 | F | GTCTGGGT | GTCTGGGT | 0.2 | | |
| Clinical Distribution | UP021 | CA | 99 | M | GGCTGTGC | GGCTGGGC | 0.4 | | |
| Edit Pathway | UP022 | CA | 99 | M | GGCTGGAC | GGCTGGAC | 0.3 | | |
| MultiGene | OR001 | AS | 99 | M | dCCCTGGGC | GGTTGTGC | 0.2 | | |
| Clinical Trial Cohorts | OR002 | AS | 99 | M | GGCTGGGC | GGCTGGGC | 0.3 | | |
| Expression | OR004 | AS | 99 | F | GCCTGGGC | GCCTGGGC | 0.2 | | |
| Assay Data | OR006 | AS | 99 | F | GGCTGGGC | GGCTGGAC | 0.1 | | |
| References | WT003 | CA | 99 | F | GGCTGGGC | GGTTGTGC | 0.2 | | |
| | WT005 | CA | 99 | M | GGCTGGGC | GGCTGGGC | 0.2 | | |
| | WT007 | CA | 99 | M | GGCTGTGC | GGTTGTGC | 0.4 | | |
| | UP012 | CA | 99 | F | GGCTAGGC | GGCTGGAC | 0.1 | | |
| | UP135 | CA | 99 | M | GCCTGGGC | GGCTGGAC | 0.2 | | |

FIG. 9



12 / 62

FIG. 10



13/62

FIG. 11

DecoGen Browser: CYP2D6

File Edit Help

GEMSAIANCE PHARMACEUTICAL

Pathways

Gene Description

Gene Structure

mRNA Structure

Protein Structure

HAP Frequencies

Haplotype Frequency vs. Ethnicity View

+ - Recalculate View Summary

Polymorphism: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☒ 8 ☐ 9

Details of the ethnic distribution as a function of subject haplotypes

3 Columns are given for each Ethnogeographic group:
Total number sampled with HAP pair
Fraction of the ethnogeographic group with that HAP pair
Fraction expected under Hardy-Weinberg equilibrium for that HAP pair

| HAP 1 | HAP 2 | N | %Pop. | Caucasian | African American | Hispanic/Latino | As |
|-----------|-----------|----|-------|----------------|------------------|-----------------|----|
| *C*****G* | *C*****G* | 23 | 50% | 18 56.3% 37.9% | 0 0.0% 0.6% | 0 0.0% 0.0% | 5 |
| *T*****G* | *C*****G* | 2 | 4% | 2 6.3% 18.9% | 0 0.0% 2.4% | 0 0.0% 0.0% | 0 |
| *T*****G* | *T*****G* | 4 | 8% | 4 12.5% 2.4% | 0 0.0% 2.4% | 0 0.0% 0.0% | 0 |
| *C*****A* | *C*****G* | 5 | 10% | 4 12.5% 25.2% | 0 0.0% 2.4% | 0 0.0% 0.0% | 1 |
| *C*****A* | *C*****A* | 3 | 6% | 3 9.4% 4.2% | 0 0.0% 2.4% | 0 0.0% 0.0% | 0 |
| *T*****A* | *C*****G* | 1 | 2% | 0 0.0% 3.2% | 1 12.5% 9.5% | 0 0.0% 0.0% | 0 |
| *T*****A* | *T*****G* | 2 | 4% | 0 0.0% 0.8% | 2 25.0% 18.9% | 0 0.0% 0.0% | 0 |
| *T*****A* | *C*****A* | 3 | 6% | 1 3.1% 1.1% | 2 25.0% 18.9% | 0 0.0% 0.0% | 0 |
| *T*****A* | *T*****A* | 3 | 6% | 0 0.0% 0.1% | 3 37.5% 37.9% | 0 0.0% 0.0% | 0 |

Edit Pathway

MultiGene

Clinical Trial Cohorts

Expression

Assay Data

References

14 / 62

FIG. 12

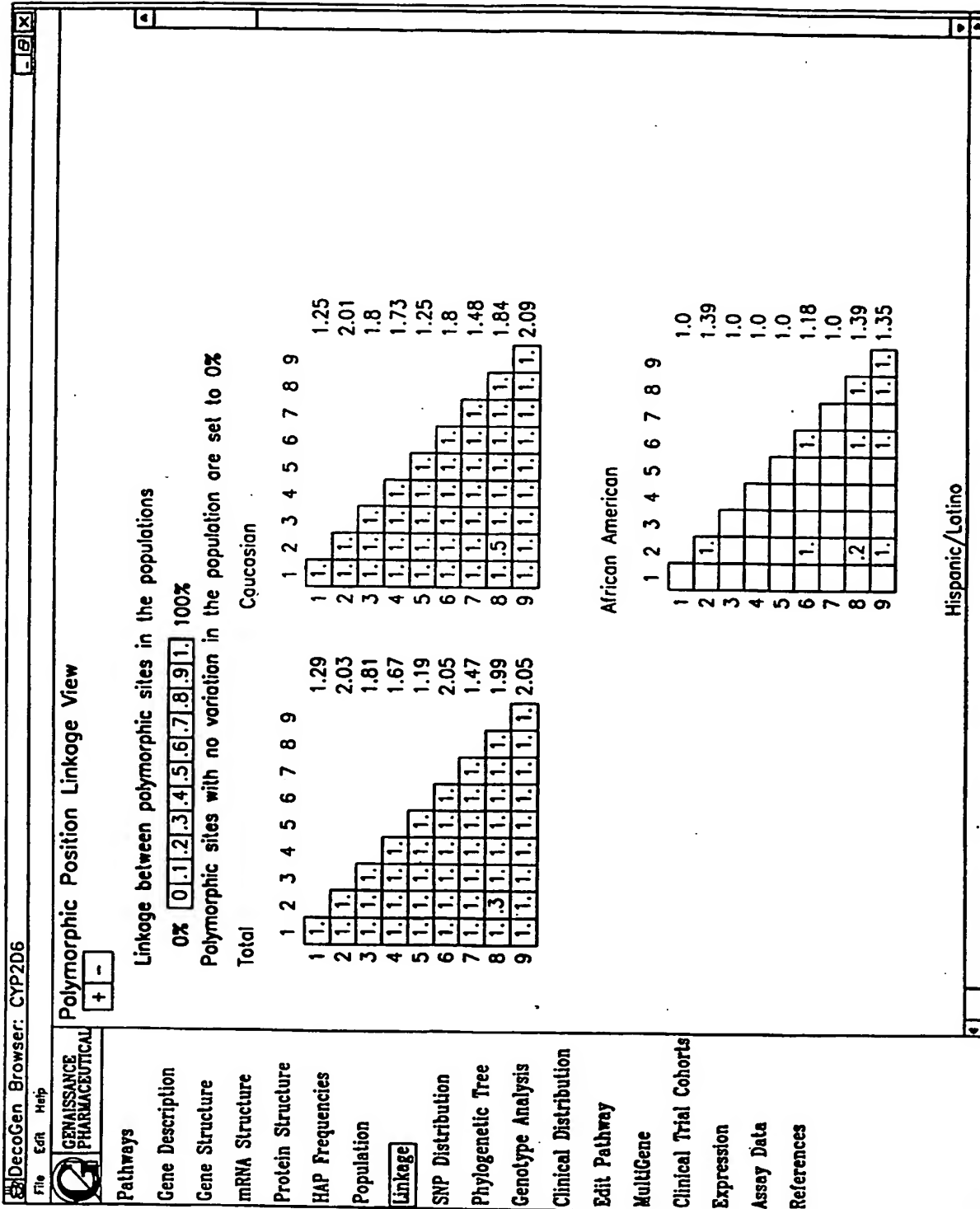
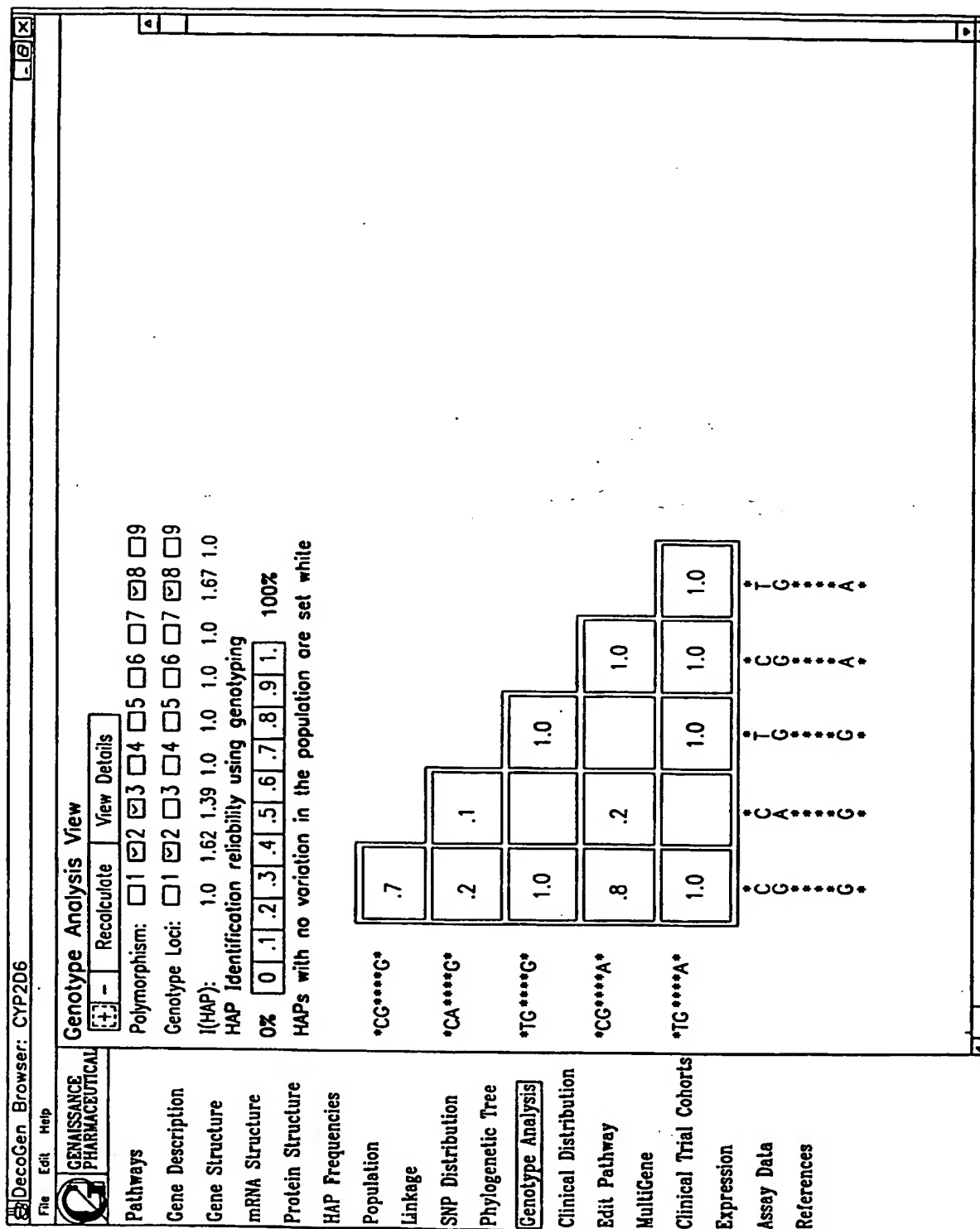


FIG. 13



16 / 62

FIG. 14

DecoGen Browser: CYP2D6

File Edit Help

GENAISSANCE PHARMACEUTICAL

Genotype Analysis View

+ - Recalculate View Optimized

Polymorphism: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☒ 8 ☐ 9

Genotype Loci: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☒ 8 ☐ 9

(HAP): 1.0 1.56 1.0 1.0 1.0 1.0 1.0 1.0 1.6 1.0

| HAP 1 | HAP 2 | N | %Pop. | Positive |
|-----------|-----------|----|-------|----------|
| *C*****G* | *C*****G* | 23 | 50% | 100% |
| *T*****G* | *C*****G* | 2 | 4% | 100% |
| *T*****G* | *T*****G* | 4 | 8% | 100% |
| *C*****A* | *C*****G* | 5 | 10% | 100% |
| *C*****A* | *C*****A* | 3 | 6% | 100% |
| *T*****A* | *C*****G* | 1 | 2% | 100% |
| *T*****A* | *T*****G* | 2 | 4% | 100% |
| *T*****A* | *C*****A* | 3 | 6% | 100% |
| *T*****A* | *T*****A* | 3 | 6% | 100% |

Pathways

Gene Description

Gene Structure

mRNA Structure

Protein Structure

HAP Frequencies

Population

Linkage

SNP Distribution

Phylogenetic Tree

Genotype Analysis

Clinical Distribution

Edit Pathway

MultiGene

Clinical Trial Cohorts

Expression

Assay Data

References

17 / 62

FIG. 15

DecoGen Browser: CYP2D6

File Edit Help

GENAISSANCE PHARMACEUTICAL

Genotype Analysis View

+ - Recalculate View Optimized

Polymorphism: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☒ 8 ☐ 9

I(HAP): 1.0 1.56 1.0 1.0 1.0 1.0 1.0 1.0 1.6 1.0 1.0

| HAP 1 | HAP 2 | Positive | Mask |
|-----------|-----------|----------|--------------------------|
| *C*****G* | *C*****G* | 100% | <input type="checkbox"/> |
| *T*****G* | *C*****G* | 100% | <input type="checkbox"/> |
| *T*****G* | *T*****G* | 100% | <input type="checkbox"/> |
| *C*****A* | *C*****G* | 100% | <input type="checkbox"/> |
| *C*****A* | *C*****A* | 100% | <input type="checkbox"/> |
| *T*****A* | *C*****G* | 100% | <input type="checkbox"/> |
| *T*****A* | *T*****G* | 100% | <input type="checkbox"/> |
| *T*****A* | *C*****A* | 100% | <input type="checkbox"/> |
| *T*****A* | *T*****A* | 100% | <input type="checkbox"/> |

Pathways

Gene Description

Gene Structure

mRNA Structure

Protein Structure

HAP Frequencies

Population

Linkage

SNP Distribution

Phylogenetic Tree

Genotype Analysis

Clinical Distribution

Edit Pathway

MultiGene

Clinical Trial Cohorts

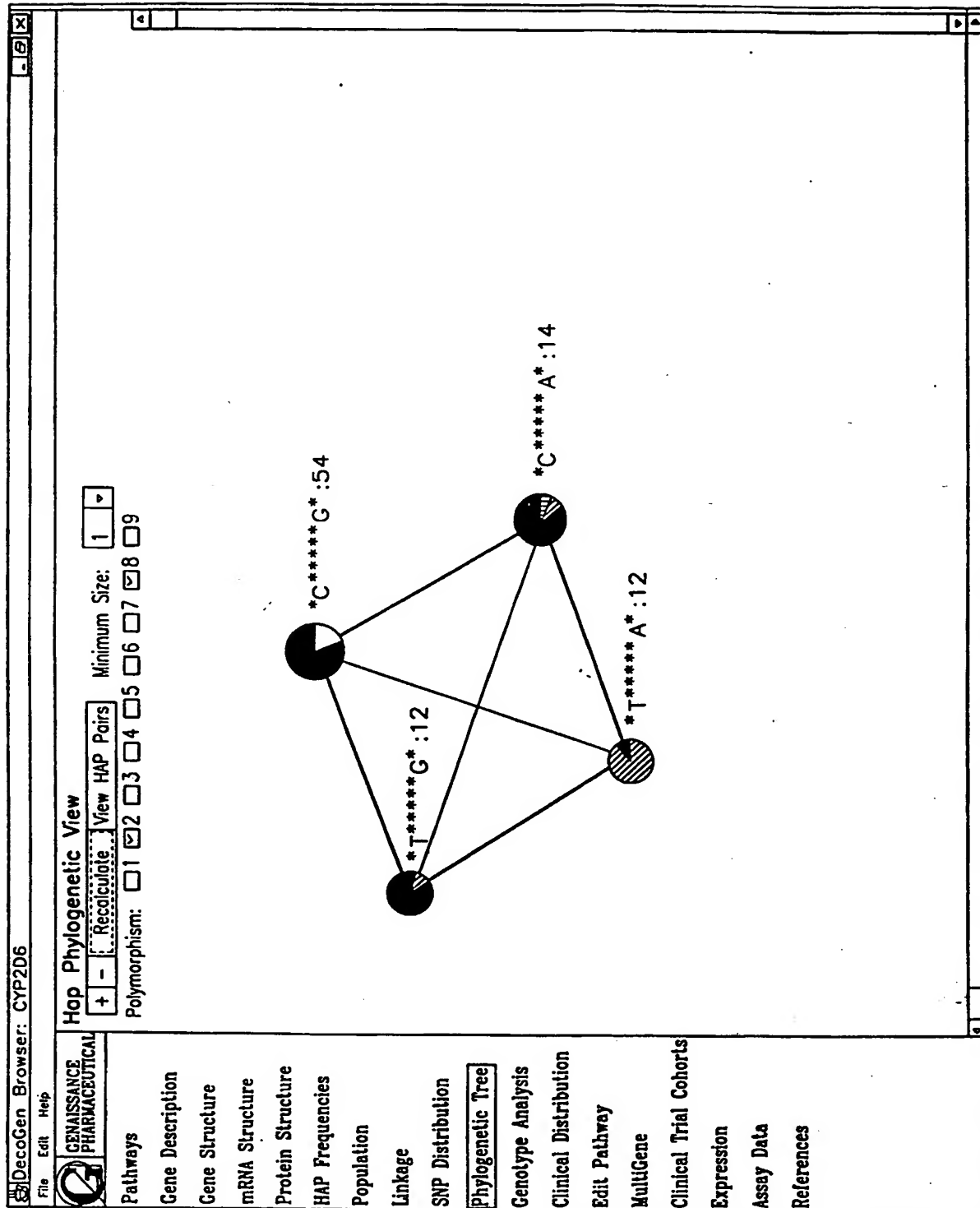
Expression

Assay Data

References

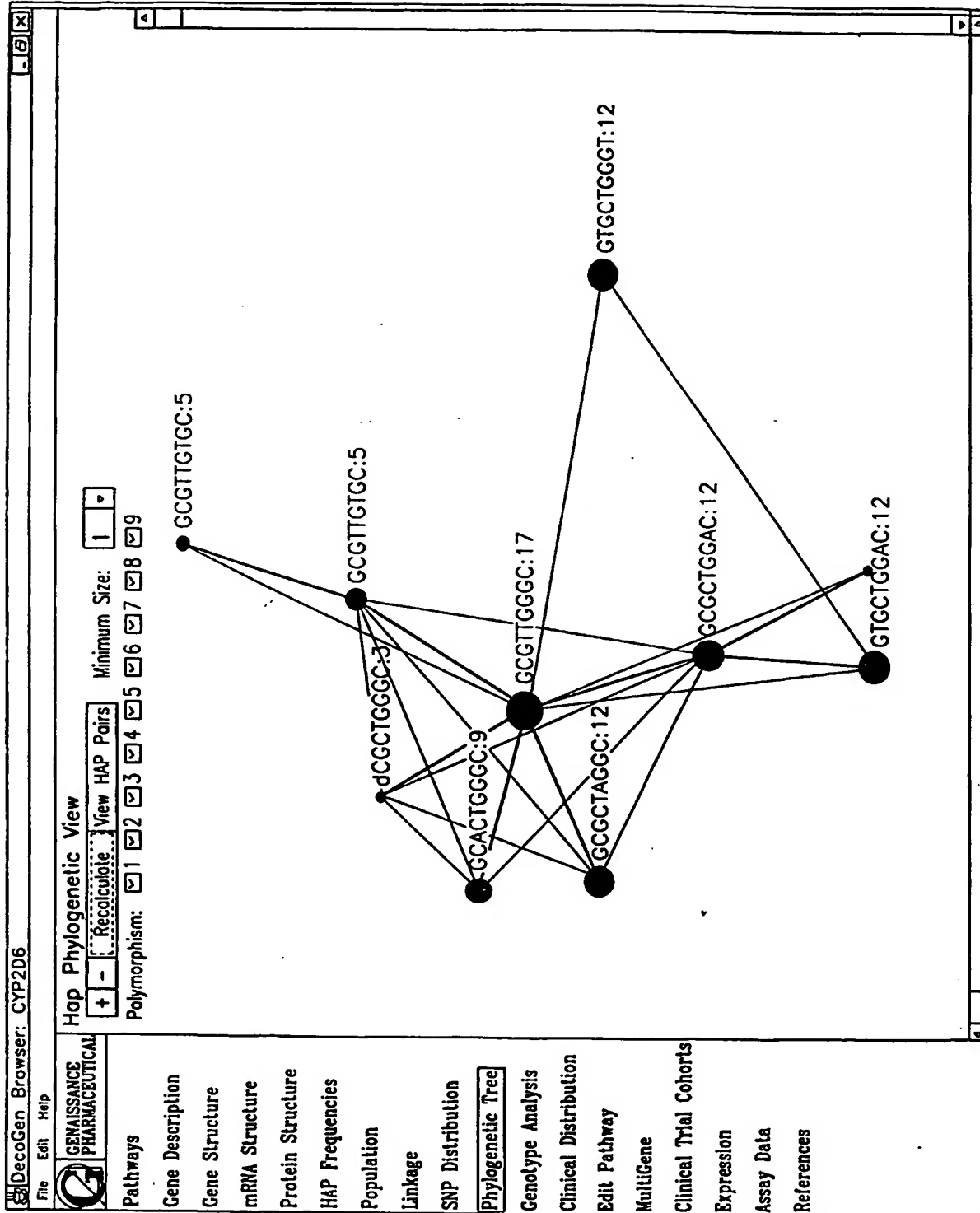
18 / 62

FIG. 16



19 / 62

FIG. 17



20 / 62

FIG. 18

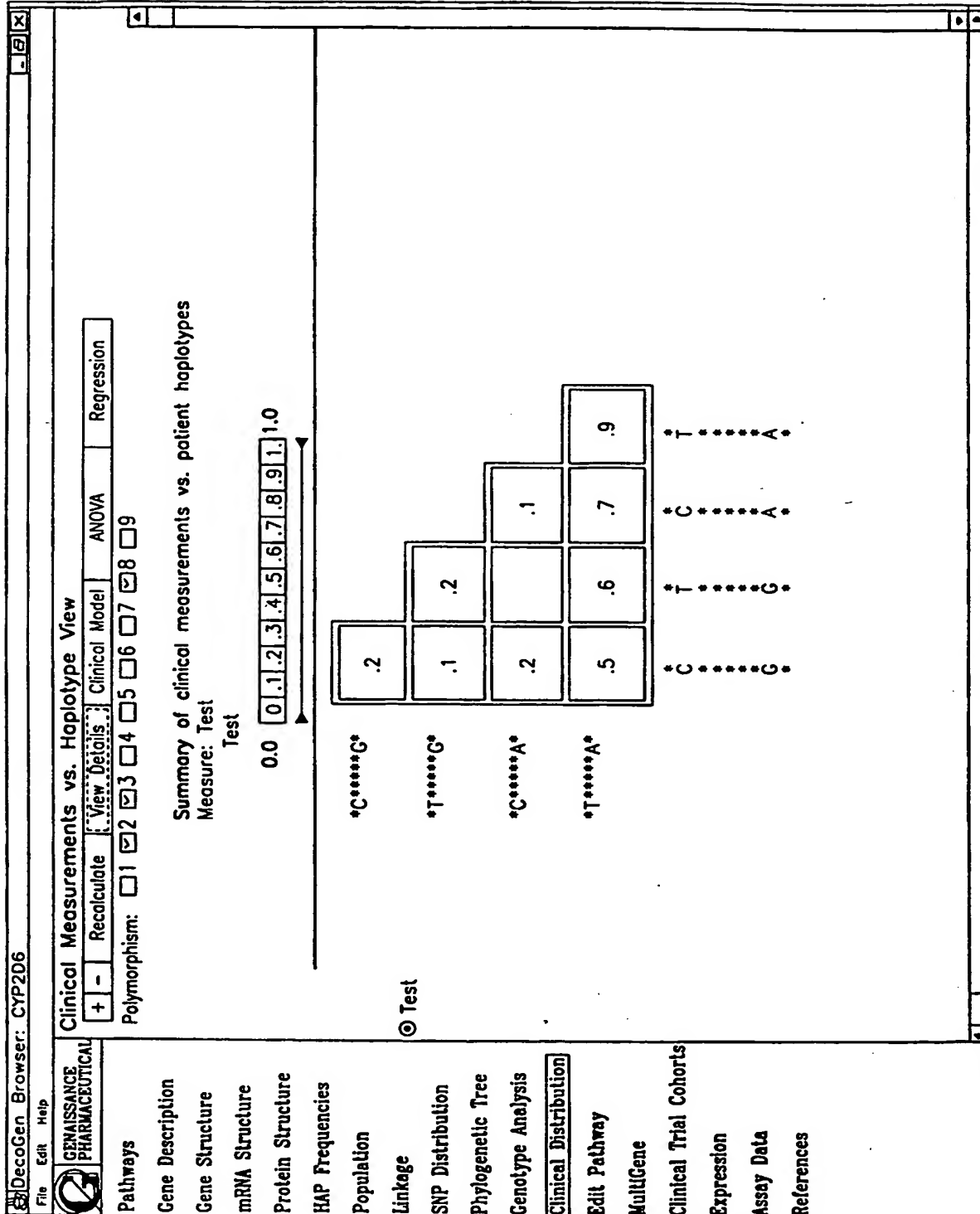
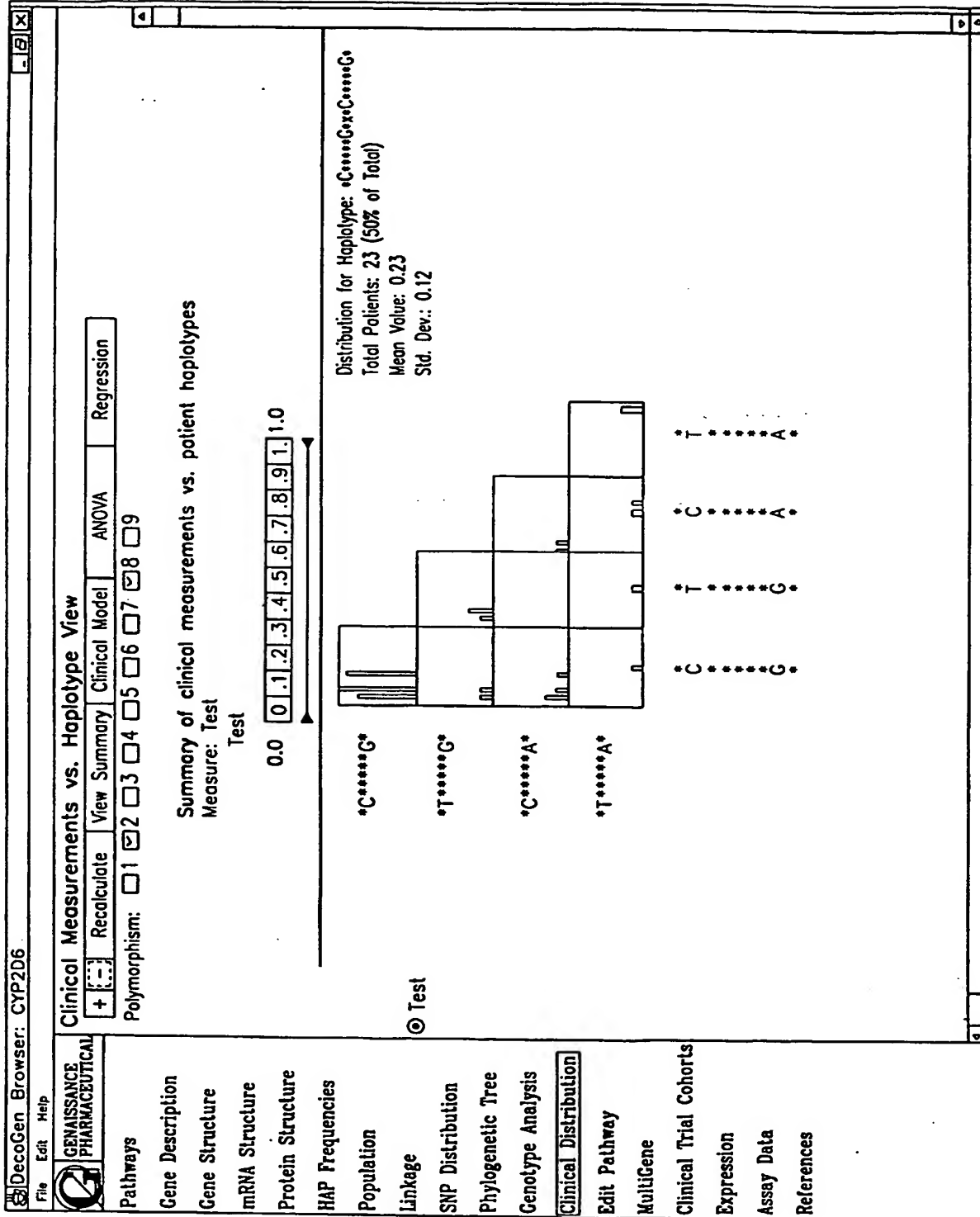


FIG. 19



22 / 62

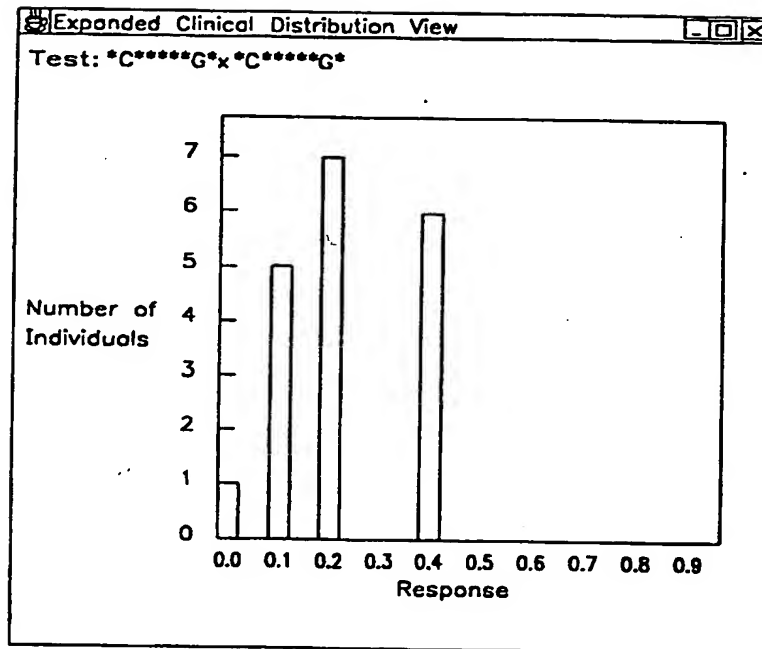
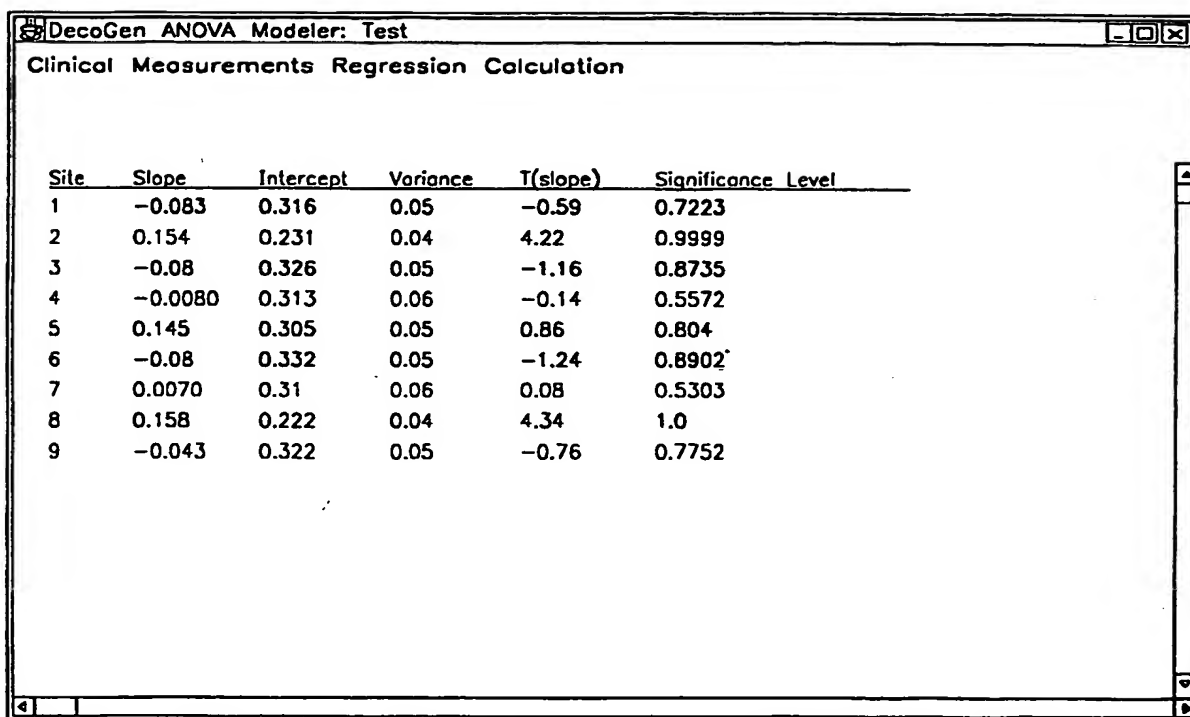


FIG. 20

23 / 62



DecoGen ANOVA Modeler: Test

Clinical Measurements Regression Calculation

| Site | Slope | Intercept | Variance | T(slope) | Significance Level |
|------|---------|-----------|----------|----------|--------------------|
| 1 | -0.083 | 0.316 | 0.05 | -0.59 | 0.7223 |
| 2 | 0.154 | 0.231 | 0.04 | 4.22 | 0.9999 |
| 3 | -0.08 | 0.326 | 0.05 | -1.16 | 0.8735 |
| 4 | -0.0080 | 0.313 | 0.06 | -0.14 | 0.5572 |
| 5 | 0.145 | 0.305 | 0.05 | 0.86 | 0.804 |
| 6 | -0.08 | 0.332 | 0.05 | -1.24 | 0.8902 |
| 7 | 0.0070 | 0.31 | 0.06 | 0.08 | 0.5303 |
| 8 | 0.158 | 0.222 | 0.04 | 4.34 | 1.0 |
| 9 | -0.043 | 0.322 | 0.05 | -0.76 | 0.7752 |

FIG. 21

24 / 62

FIG. 22

DecoGen Browser: CYP2D6

File Edit Help

CENAISSANCE PHARMACEUTICAL

Clinical Measurements vs. Haplotype View

+ - Recalculate View Distribution Clinical Model ANOVA Regression

Polymorphism: ☐ 1 ☒ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☒ 8 ☐ 9

Summary of clinical measurements vs. patient haplotypes

Measure: Test

0.0 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1.0

Test

| HAP 1 | Hap 2 | N | %Pop. | Mean | Stddev | X**2 | Q(X**2 K-3) |
|----------|----------|----|-------|------|--------|------|-------------|
| *C****G* | *C****G* | 23 | 50% | 0.24 | 0.12 | 9.17 | 0.0 (1) |
| *T****G* | *C****G* | 2 | 4% | 0.15 | 0.07 | 0.0 | 1.0 (-3) |
| *T****G* | *T****G* | 4 | 8% | 0.2 | 0.08 | 0.0 | 1.0 (-3) |
| *C****A* | *C****G* | 5 | 10% | 0.22 | 0.13 | 0.8 | 1.0 (-2) |
| *C****A* | *C****A* | 3 | 6% | 0.13 | 0.15 | 0.0 | 1.0 (-3) |
| *T****A* | *C****G* | 1 | 2% | 0.5 | 0.0 | 0.0 | 1.0 (-3) |
| *T****A* | *T****G* | 2 | 4% | 0.55 | 0.07 | 0.0 | 1.0 (-3) |
| *T****A* | *C****A* | 3 | 6% | .6 | 0.1 | 0.0 | 1.0 (-3) |
| *T****A* | *T****A* | 3 | 6% | 0.93 | 0.06 | 0.0 | 1.0 (-3) |

Test

Test

Pathways

Gene Description

Gene Structure

mRNA Structure

Protein Structure

HAP Frequencies

Population

Linkage

SNP Distribution

Phylogenetic Tree

Genotype Analysis

Clinical Distribution

Edit Pathway

MultiGene

Clinical Trial Cohorts

Expression

Assay Data

References

25/62

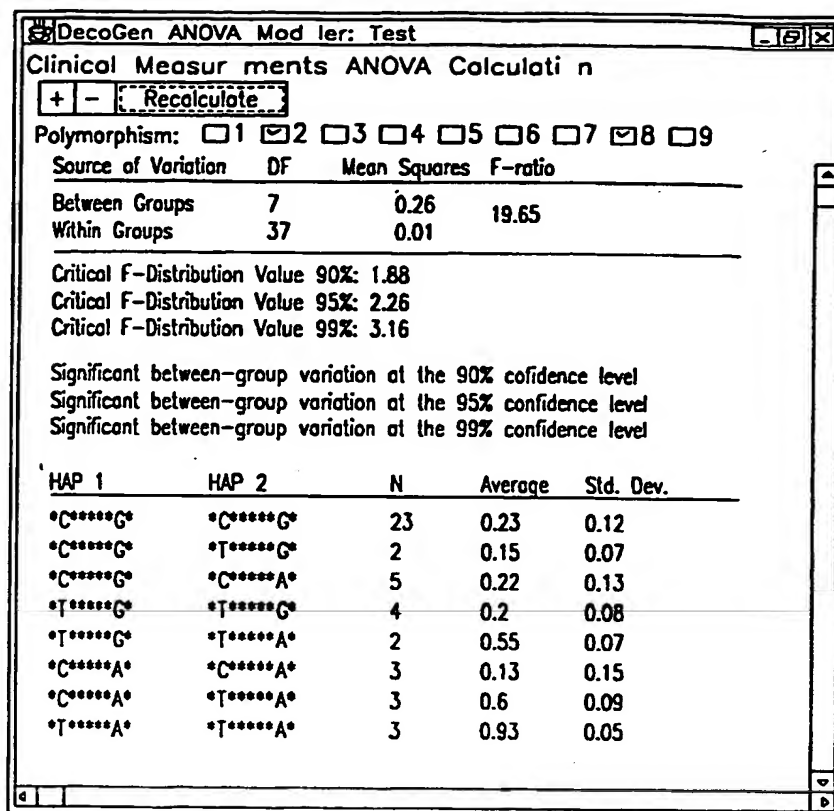


FIG. 23

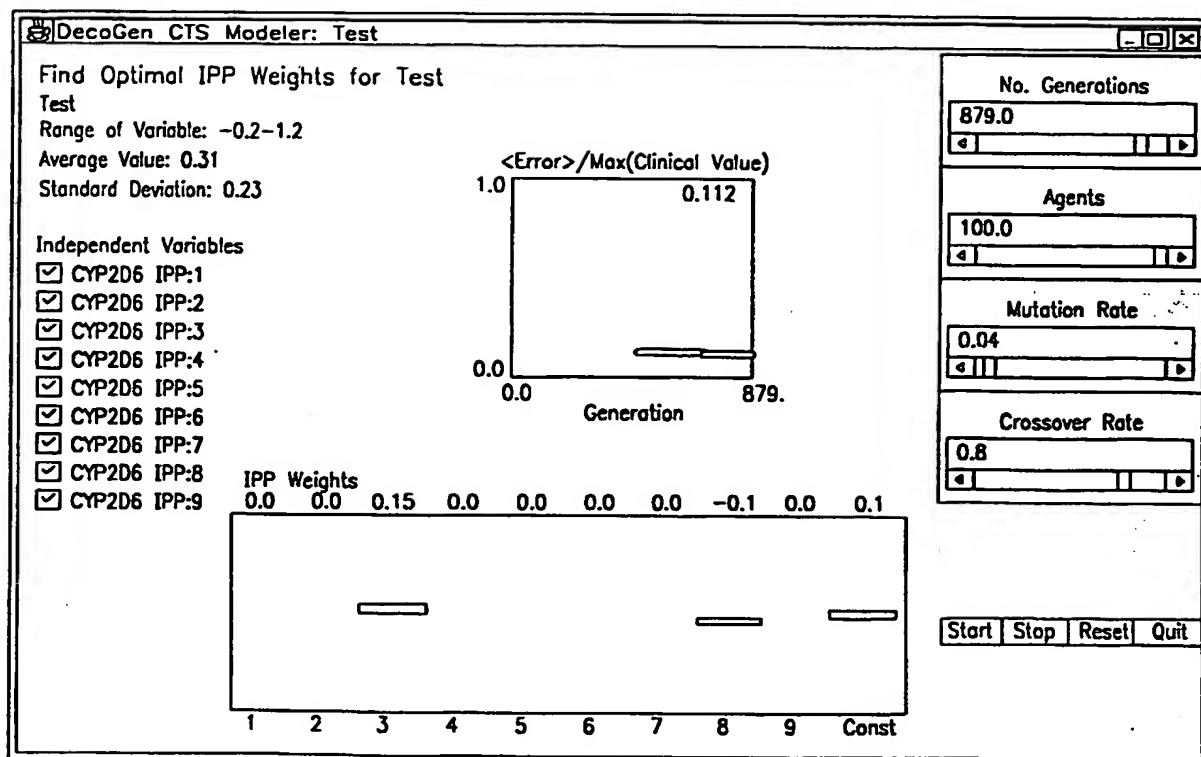


FIG. 24

26 / 62

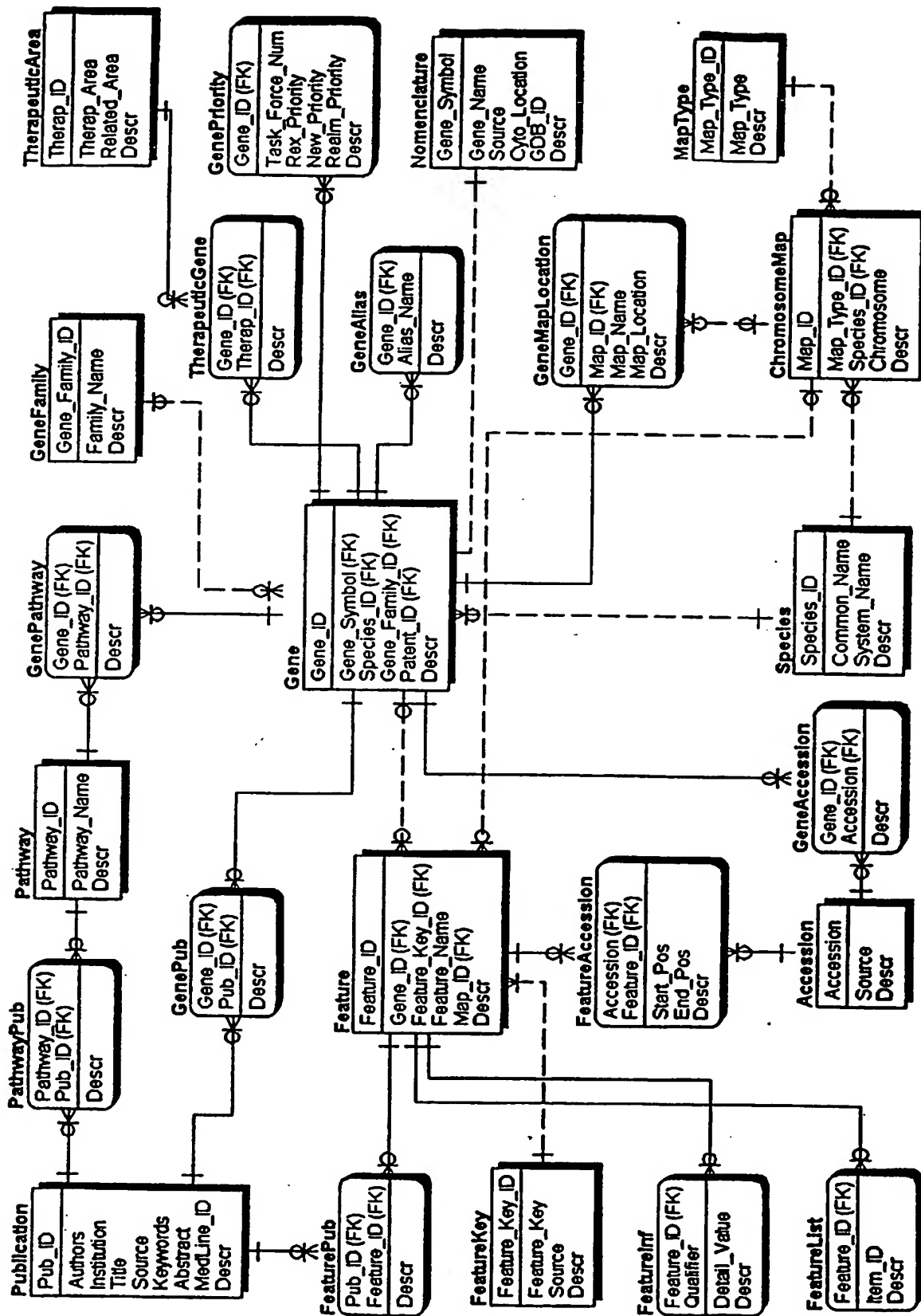
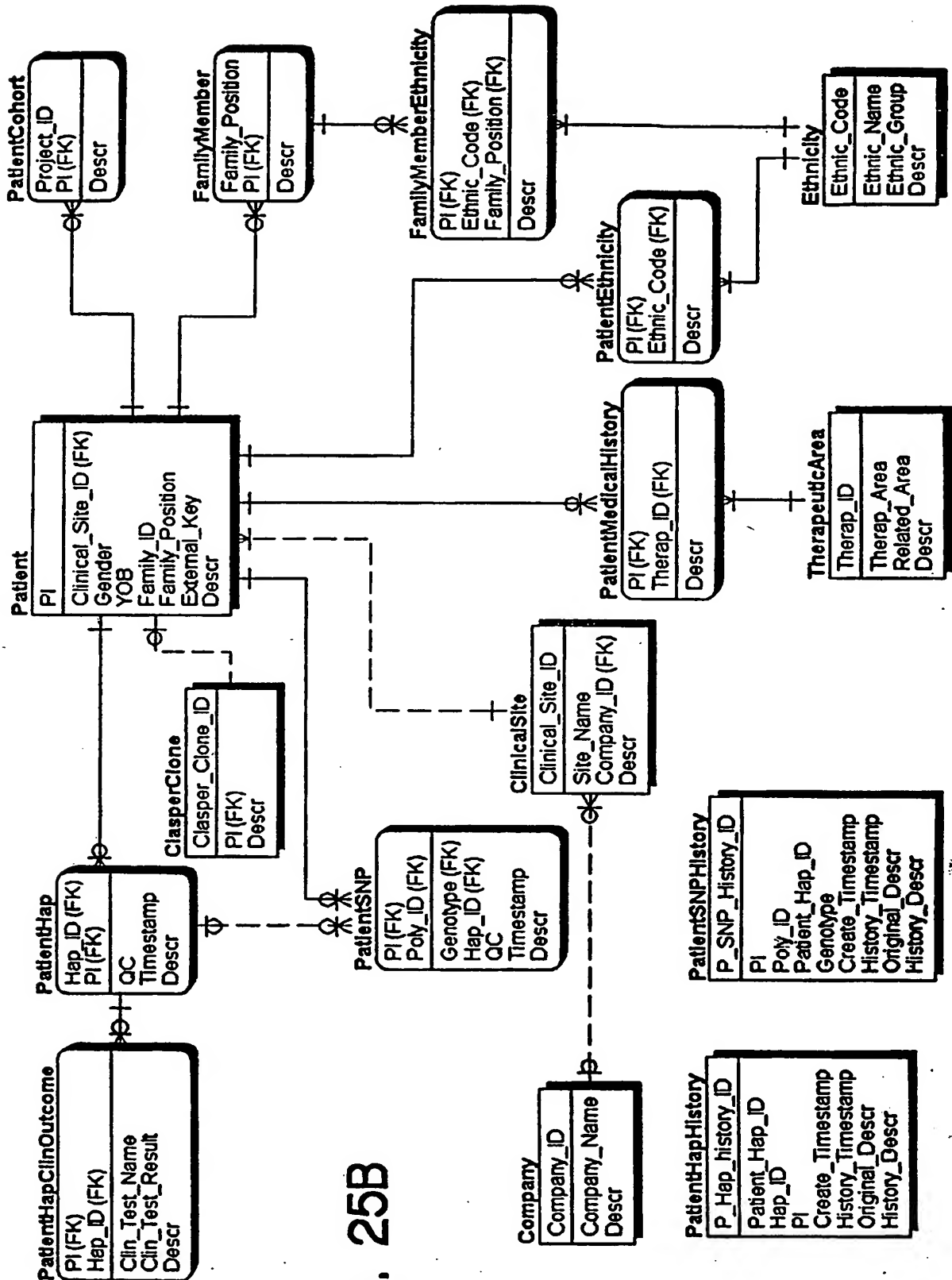


FIG. 25A

27 / 62



28 / 62

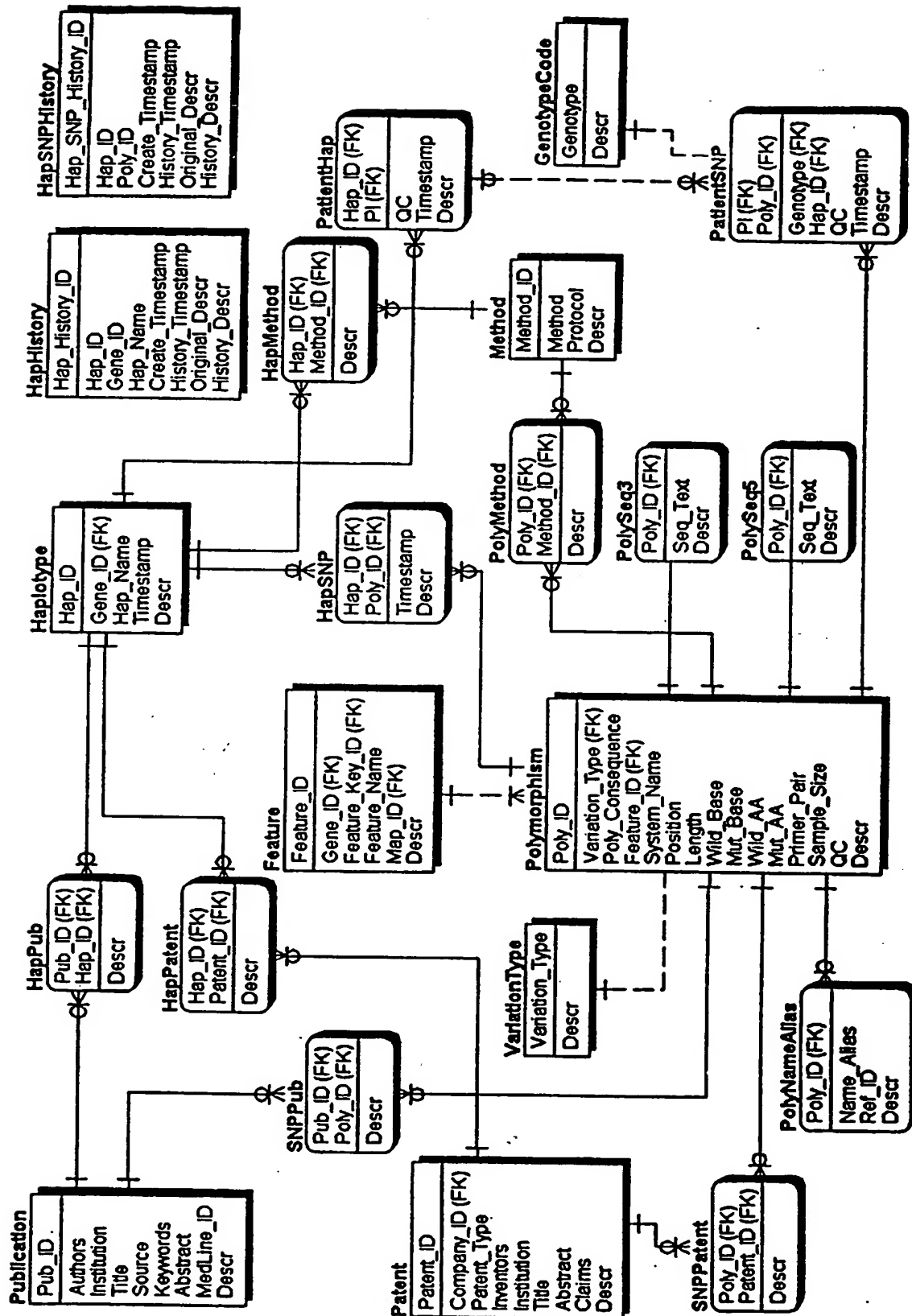


FIG. 25C

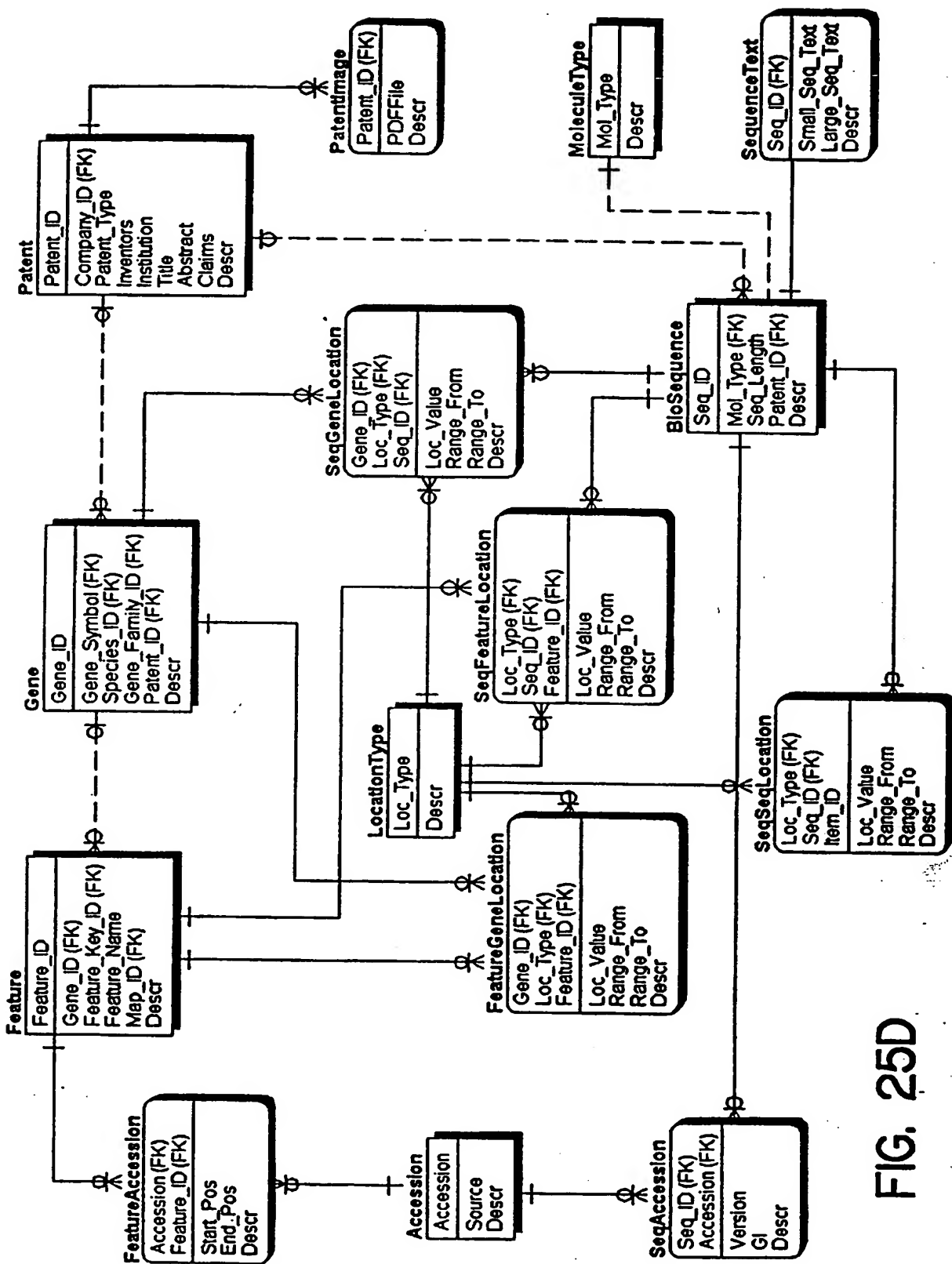


FIG. 25D

30 / 62

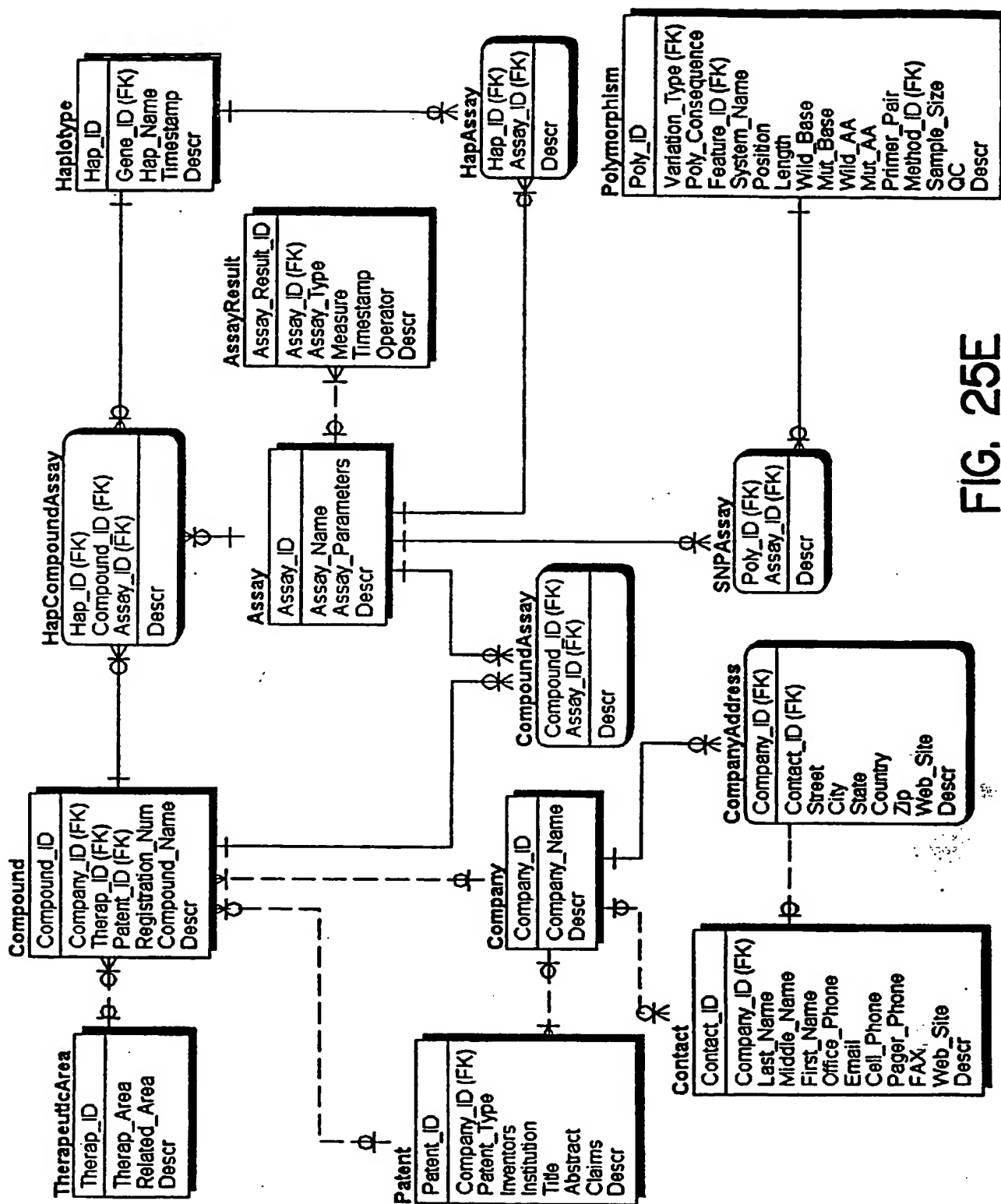
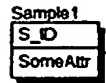
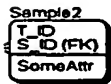


FIG. 25E

31 / 62

Legend of Figures:

Rectangle Boxes: Tables in the database.



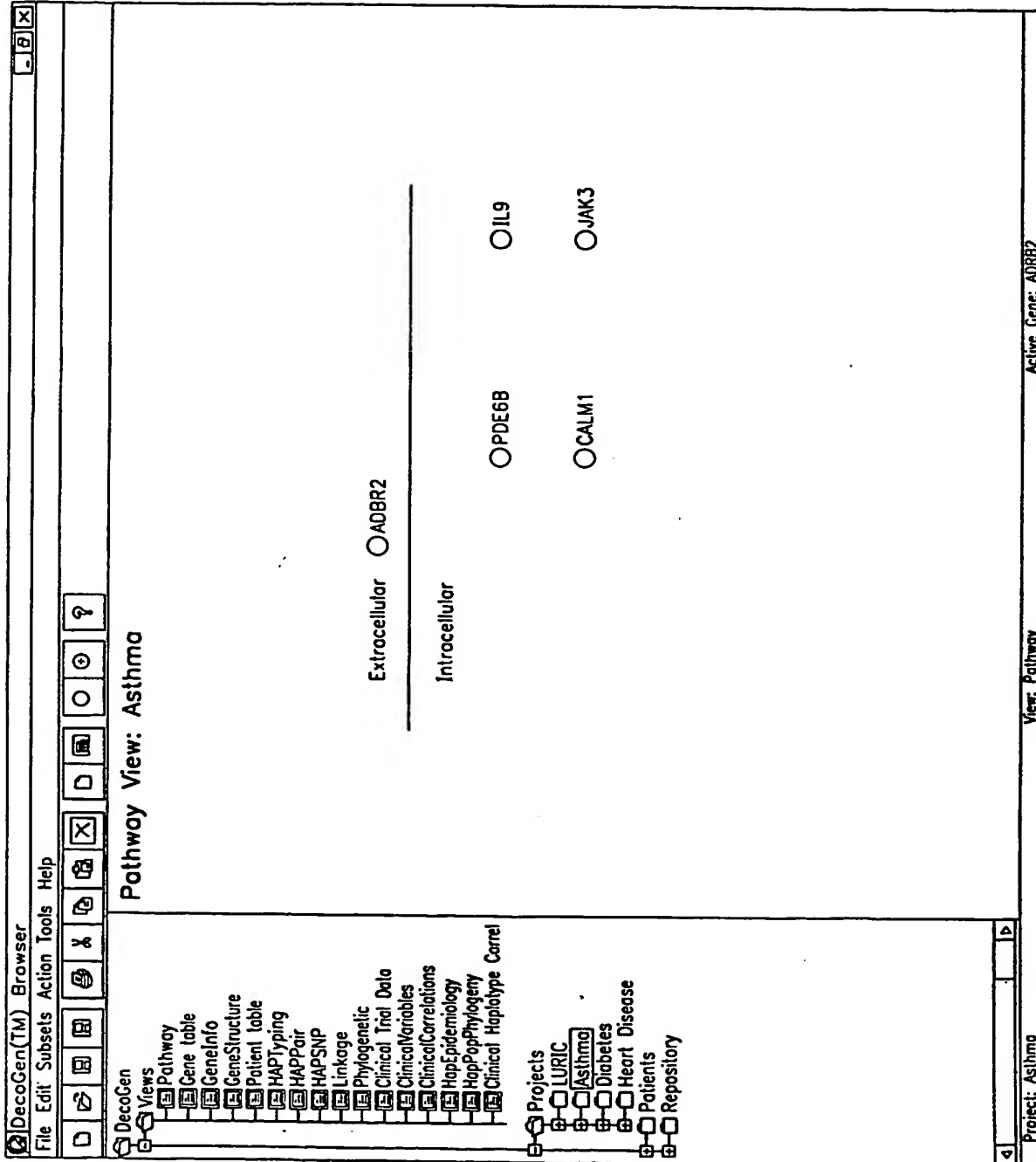
Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: ————* Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: ————* Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: ————* Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 8: - - - - * Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.
- 10: |——— Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: ⊕ ——— Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.
- 14: |———* Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

FIG. 25F

32 / 62

FIG. 26



33 / 62

FIG. 27

DecoGen(TM) Browser
File Edit Subsets Action Tools Help

Views
☒ Pathway
☒ Gene table
☒ GeneInfo
☒ GeneStructure
☒ Patient table
☒ HAPTyping
☒ HAPPair
☒ HAPSNP
☒ Linkage
☒ Phylogenetic
☒ Clinical Trial Data
☒ ClinicalVariables
☒ ClinicalCorrelations
☒ HapEpidemiology
☒ HapPopPhylogeny
☒ Clinical Haplotype Correl

Projects
☐ LURIC
☐ Asthma
☐ Diabetes
☐ Heart Disease
☐ Patients
☐ Repository

Gene Description View

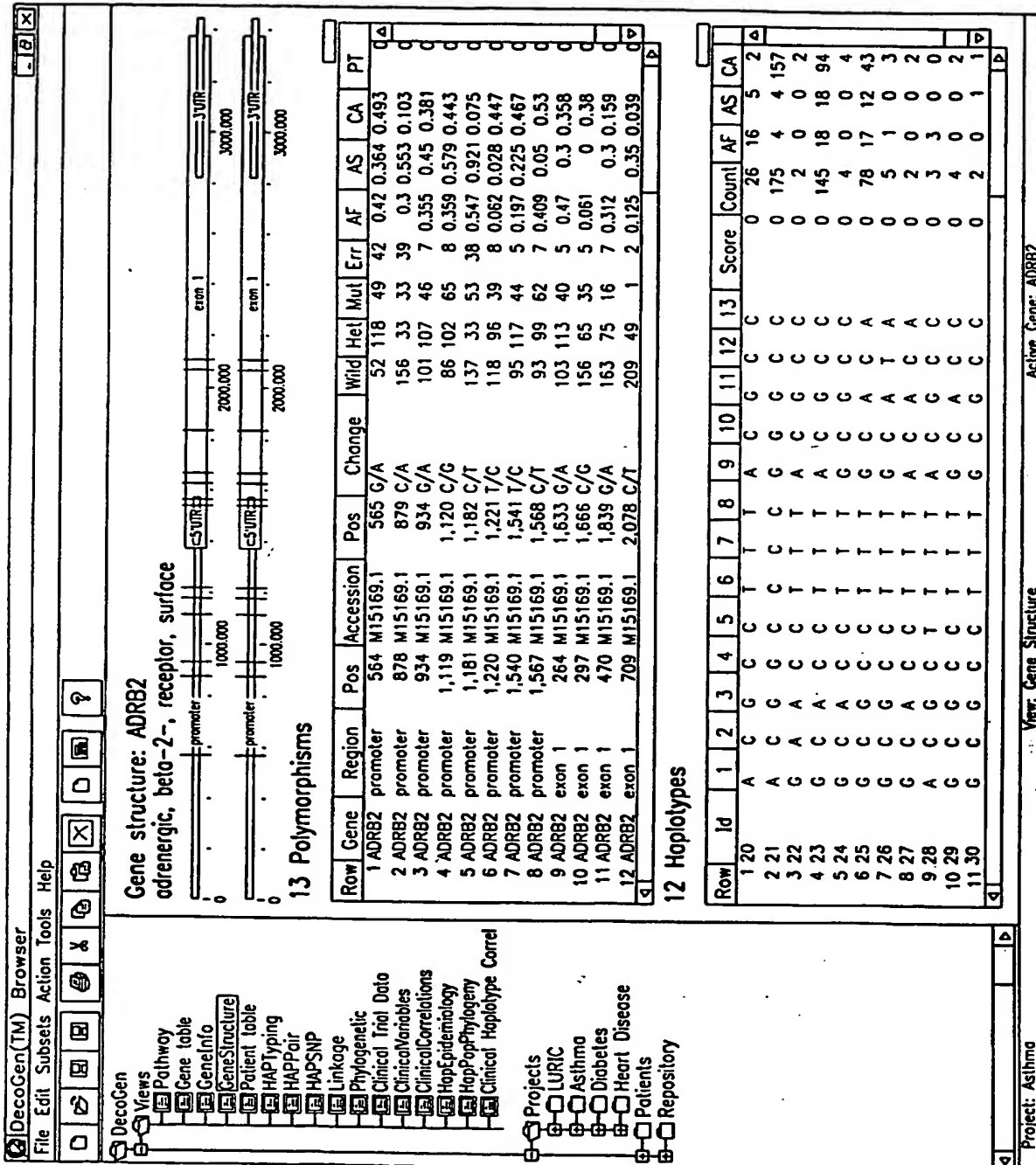
| | |
|--------------------------------|--|
| Name | ADRB2 |
| Definition | adrenergic, beta-2-, receptor, surface |
| Function | Function |
| Organism | Human |
| Length | 3451 |
| No. Features | 5 |
| Population Size | 261 |
| No. Haplotypes | 12 |
| No. SNPs | 13 |
| Nucleotide Polymorphism (helo) | 7.9E-4 +/-3.9E-4 |
| Nucleotide Diversity (pi) | 4.6E-4 +/-2.8E-4 |

Project: Asthma View: GeneInfo Active Gene: ADRB2

34 / 62

10'019242

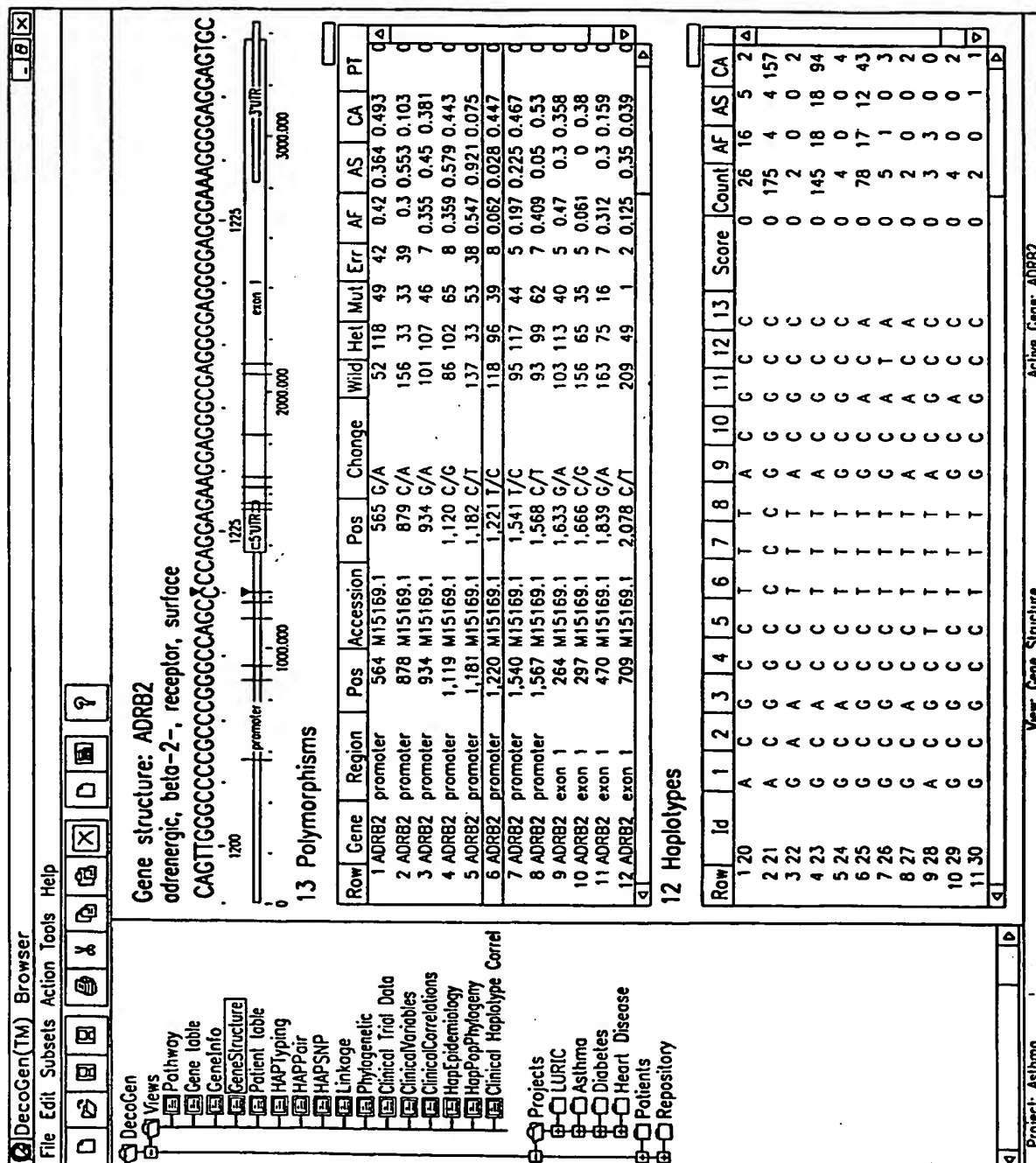
FIG. 28A



35 / 62

10/019242

FIG. 28B



36 / 62

10/019242

FIG. 29A

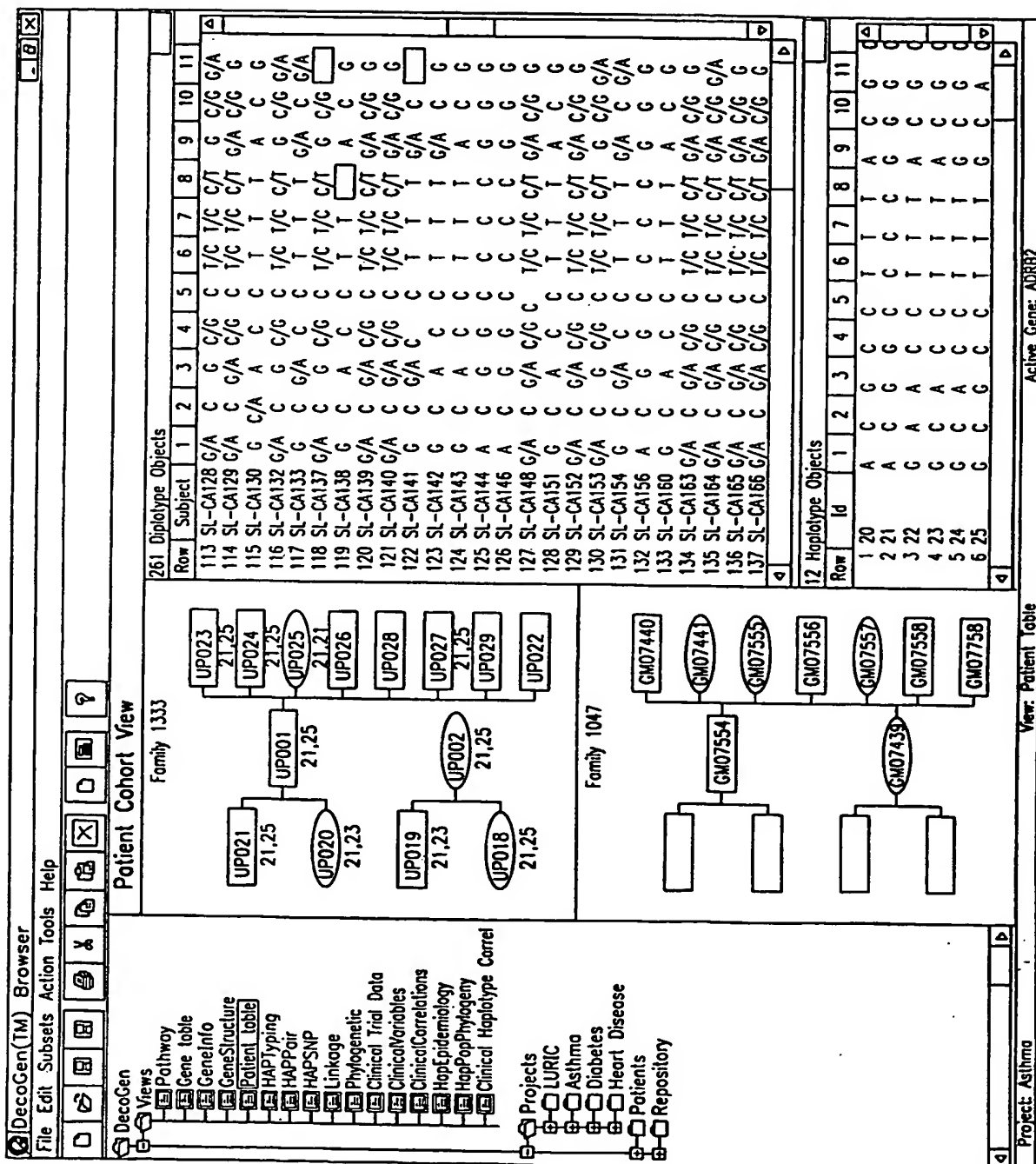


FIG. 29B

DecoGen(TM) Browser

File Edit Subsets Action Tools Help

?

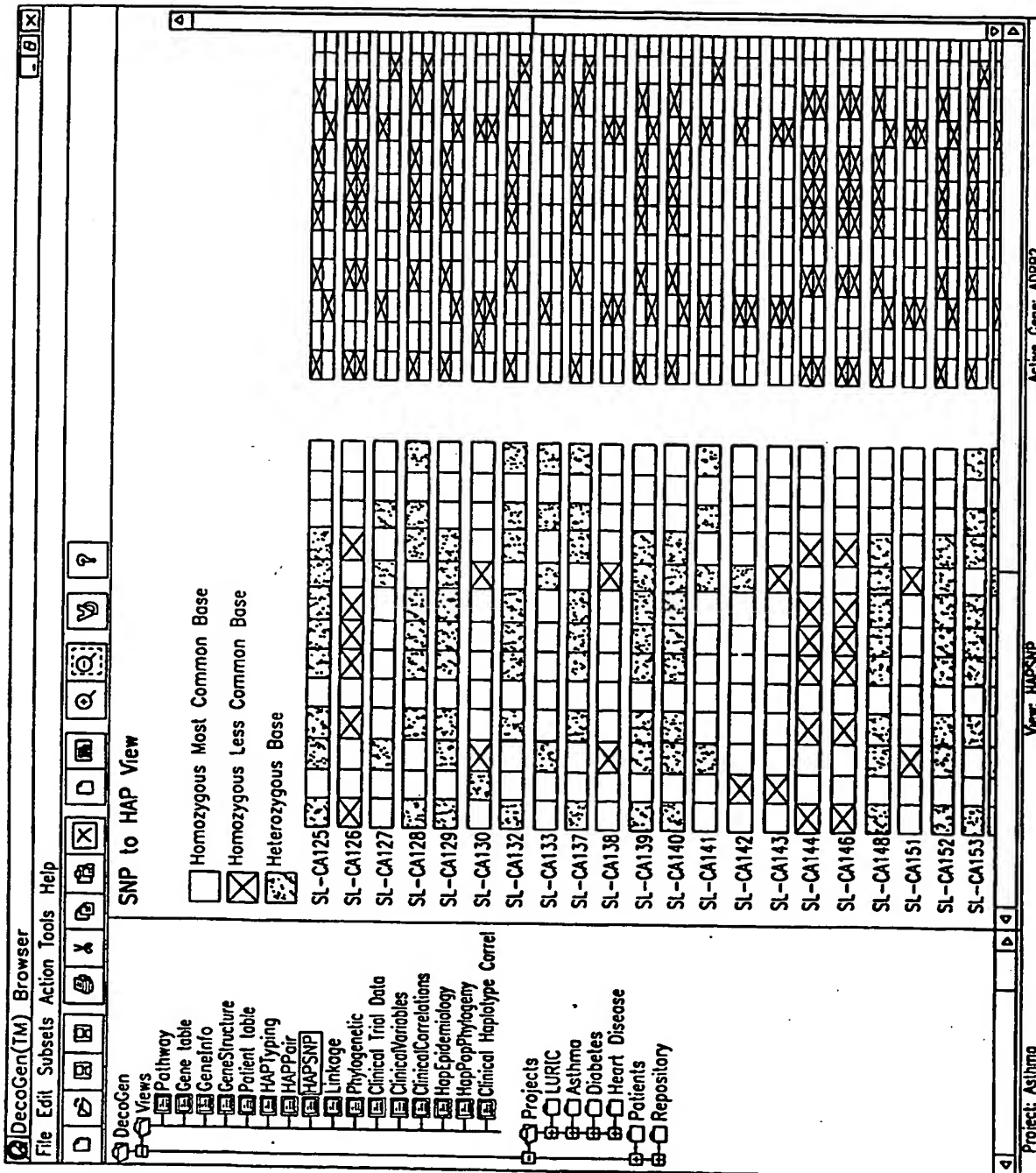
Clinical Trial Data

182 Patient/Mesurement Objects

| Row | Patient | Severity | Skin Tes... | FVC LP... | FVC ZP... | FEV1 L... | FEV1 %... | FEV1/FV... | FEF PRE | FEF ZP... | PVC |
|-----|----------|----------|-------------|-----------|-----------|-----------|-----------|------------|---------|-----------|------|
| 1 | SL-AA131 | 2.0 | 1.0 | 1.88 | 58.0 | 1.28 | 52.0 | 68.0 | 0.83 | 49.0 | 1.81 |
| 2 | SL-AA134 | 2.0 | 1.0 | 2.01 | 54.0 | 0.96 | 34.0 | 48.0 | 0.45 | 12.0 | 2.2 |
| 3 | SL-AA136 | 0.0 | 0.0 | 2.56 | 89.0 | 2.22 | 93.0 | 87.0 | 3.2 | 91.0 | 2.5 |
| 4 | SL-AA150 | 2.0 | 1.0 | 1.4 | 50.0 | 0.6 | 27.0 | 43.0 | 0.22 | 7.0 | 1.5 |
| 5 | SL-AA155 | 2.0 | 1.0 | 1.77 | 40.0 | 0.98 | 27.0 | 55.0 | 0.61 | 16.0 | 2.2 |
| 6 | SL-AA159 | 2.0 | 1.0 | 2.89 | 66.0 | 1.71 | 51.0 | 59.0 | 0.9 | 20.0 | 4.4 |
| 7 | SL-AA195 | 1.0 | 1.0 | 4.28 | 96.0 | 2.7 | 79.0 | 63.0 | 1.48 | 33.0 | 5.2 |
| 8 | SL-AA211 | 1.0 | 1.0 | 3.44 | 91.0 | 1.97 | 66.0 | 57.0 | 1.39 | 32.0 | 5.5 |
| 9 | SL-AA227 | 2.0 | 0.0 | 1.93 | 54.0 | 0.96 | 37.0 | 49.0 | 0.35 | 11.0 | 2.5 |
| 10 | SL-AA253 | 1.0 | 1.0 | 3.0 | 96.0 | 2.01 | 70.0 | 57.0 | 0.99 | 25.0 | 3.8 |
| 11 | SL-AA270 | NP | NP | NP | NP | NP | NP | NP | NP | NP | NP |
| 12 | SL-AA275 | NP | NP | NP | NP | NP | NP | NP | NP | NP | NP |
| 13 | SL-CA101 | 1.0 | 1.0 | 2.17 | 85.0 | 1.92 | 64.0 | 71.0 | 1.33 | 38.0 | 3.2 |
| 14 | SL-CA103 | 2.0 | 1.0 | 3.56 | 59.0 | 2.16 | 46.0 | 61.0 | 1.13 | 18.0 | 4.1 |
| 15 | SL-CA104 | 2.0 | 0.0 | 2.76 | 57.0 | 1.46 | 39.0 | 53.0 | 0.59 | 16.0 | 3.4 |
| 16 | SL-CA105 | 2.0 | 0.0 | 1.99 | 62.0 | 1.11 | 46.0 | 57.0 | 0.55 | 24.0 | 2.3 |
| 17 | SL-CA106 | 0.0 | 1.0 | 3.46 | 82.0 | 2.69 | 83.0 | 57.0 | 2.28 | 51.0 | 4.4 |
| 18 | SL-CA107 | 0.0 | 1.0 | 3.82 | 113.0 | 2.59 | 83.0 | 78.0 | 1.7 | 46.0 | 3.9 |
| 19 | SL-CA108 | NP | NP | NP | NP | NP | NP | NP | NP | NP | NP |
| 20 | SL-CA109 | 1.0 | 1.0 | 2.63 | 93.0 | 1.7 | 7.0 | 64.5 | 0.89 | 25.0 | 2.8 |
| 21 | SL-CA110 | 0.0 | 1.0 | 4.56 | 114.0 | 3.18 | 101.0 | 70.0 | 2.24 | 51.0 | 4.5 |
| 22 | SL-CA111 | 2.0 | 1.0 | 3.08 | 69.0 | 2.01 | 58.0 | 65.0 | 1.12 | 32.0 | 3.3 |
| 23 | SL-CA114 | 1.0 | 0.0 | 2.83 | 84.0 | 2.18 | 77.0 | 77.0 | 1.77 | 43.0 | 3.0 |
| 24 | SL-CA116 | 1.0 | 1.0 | 2.44 | 83.0 | 1.91 | 79.0 | 78.0 | 1.8 | 49.0 | 2.4 |
| 25 | SL-CA117 | 1.0 | 1.0 | 3.81 | 90.0 | 2.25 | 67.0 | 59.0 | 1.04 | 22.0 | 4.1 |
| 26 | SL-CA118 | 1.0 | 1.0 | 1.53 | 76.0 | 1.27 | 71.0 | 83.0 | 1.27 | 49.0 | 1.6 |
| 27 | SL-CA119 | NP | NP | NP | NP | NP | NP | NP | NP | NP | NP |
| 28 | SL-CA120 | 0.0 | 1.0 | 4.24 | 106.0 | 2.71 | 83.0 | 64.0 | 1.61 | 33.0 | 4.4 |
| 29 | SL-CA121 | 1.0 | 0.0 | 3.05 | 88.0 | 1.9 | 70.0 | 62.0 | 0.95 | 26.0 | 3.6 |
| 30 | SL-CA122 | 0.0 | 1.0 | 5.76 | 105.0 | 4.35 | 103.0 | 75.5 | 3.52 | 62.0 | 6.0 |
| 31 | SL-CA123 | 2.0 | 1.0 | 1.82 | 66.0 | 0.92 | 40.0 | 50.0 | 0.41 | 12.0 | 2.5 |
| 32 | SL-CA124 | 2.0 | 0.0 | 2.45 | 59.0 | 1.3 | 43.0 | 53.0 | 0.41 | 11.0 | 2.5 |
| 33 | SL-CA125 | 2.0 | 1.0 | 1.19 | 42.0 | 0.81 | 37.0 | 68.0 | 0.47 | 22.0 | 1.3 |
| 34 | SL-CA126 | 2.0 | 0.0 | 1.74 | 64.0 | 1.17 | 52.0 | 67.0 | 0.55 | 18.0 | 1.8 |
| 35 | SL-CA127 | 1.0 | 1.0 | 1.97 | 68.7 | 1.63 | 73.0 | 83.0 | 1.49 | 66.6 | 2.6 |

Active Gene: ADRB2

FIG. 30



39 / 62

FIG. 3I

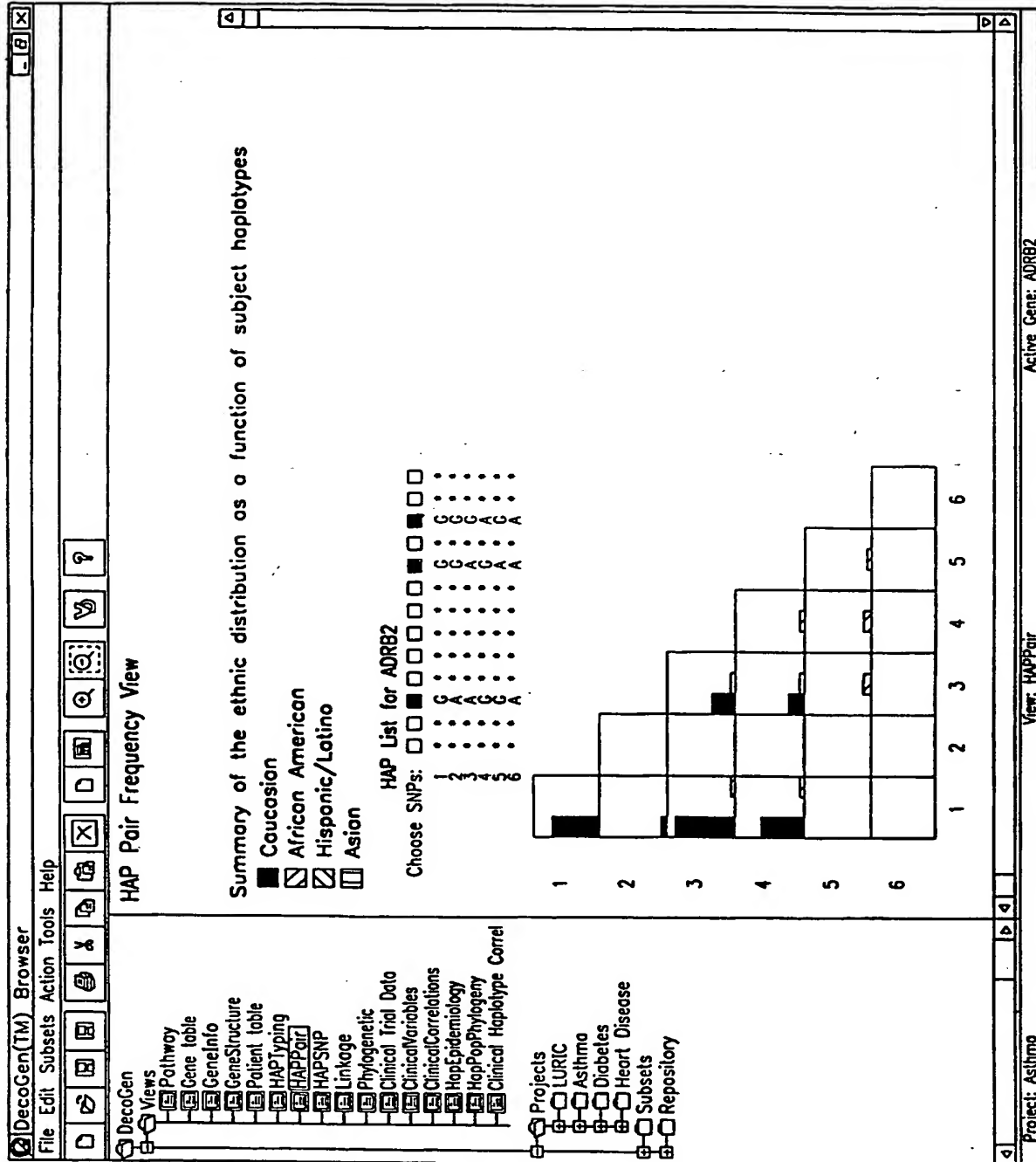
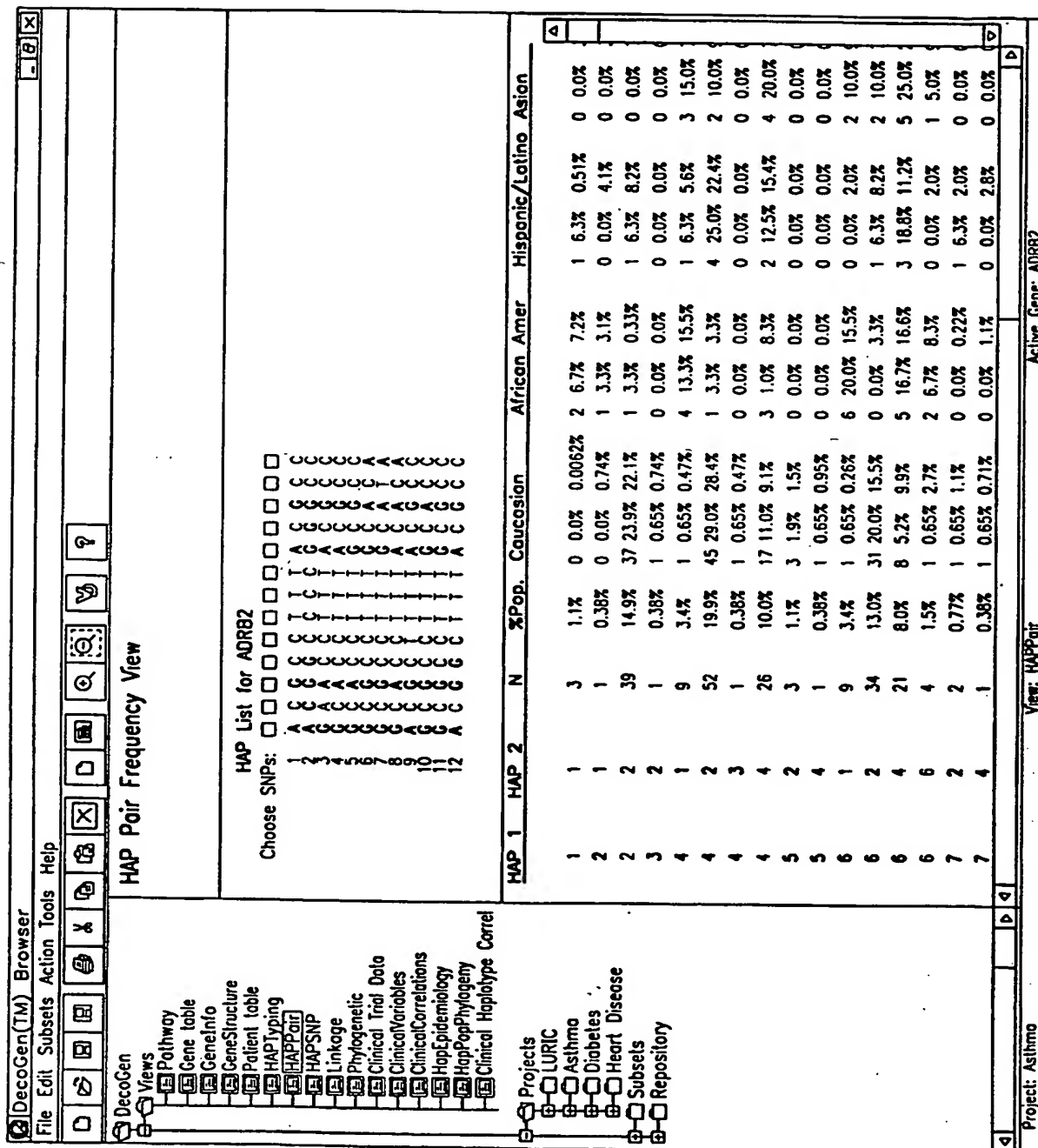
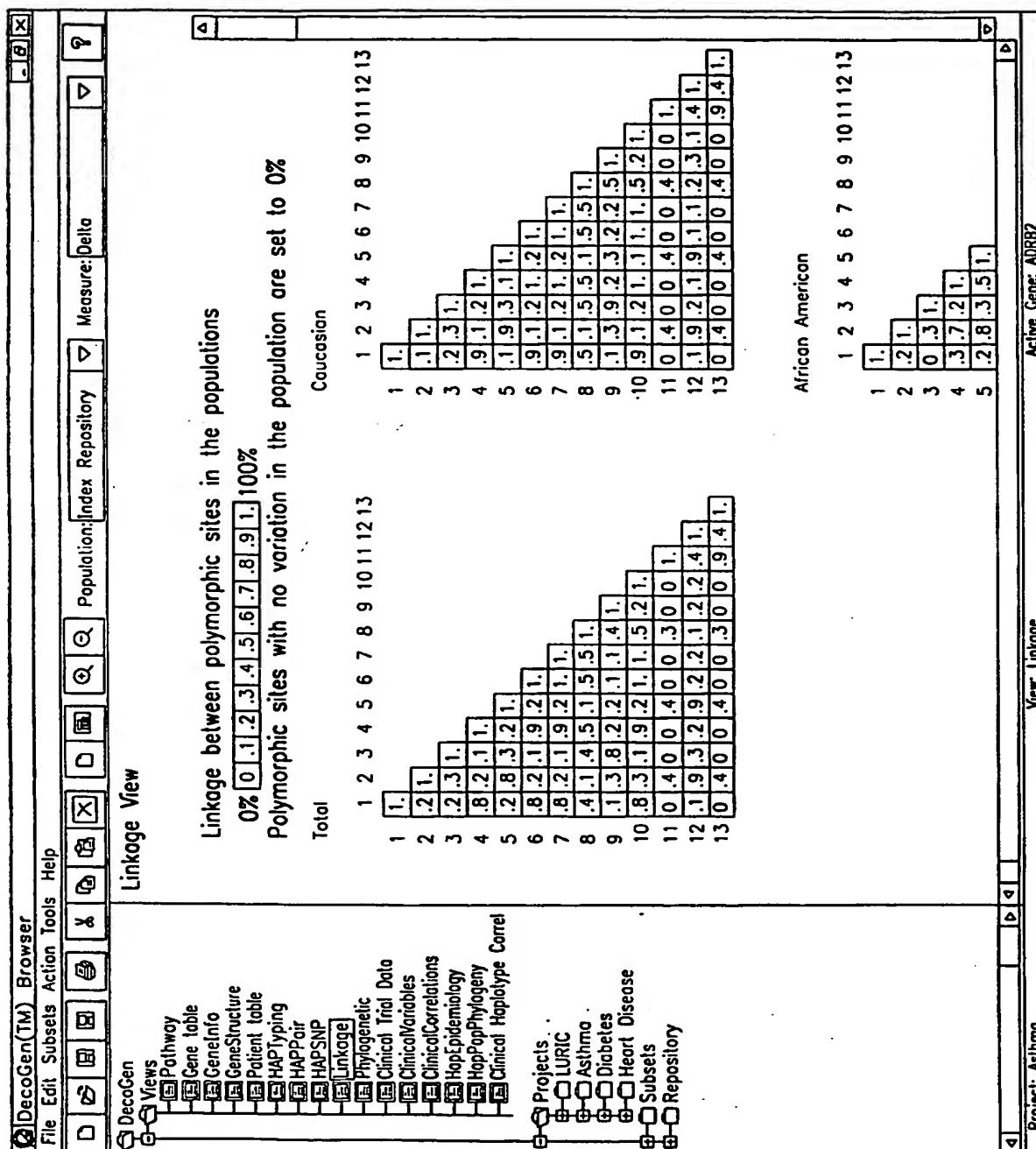


FIG. 32



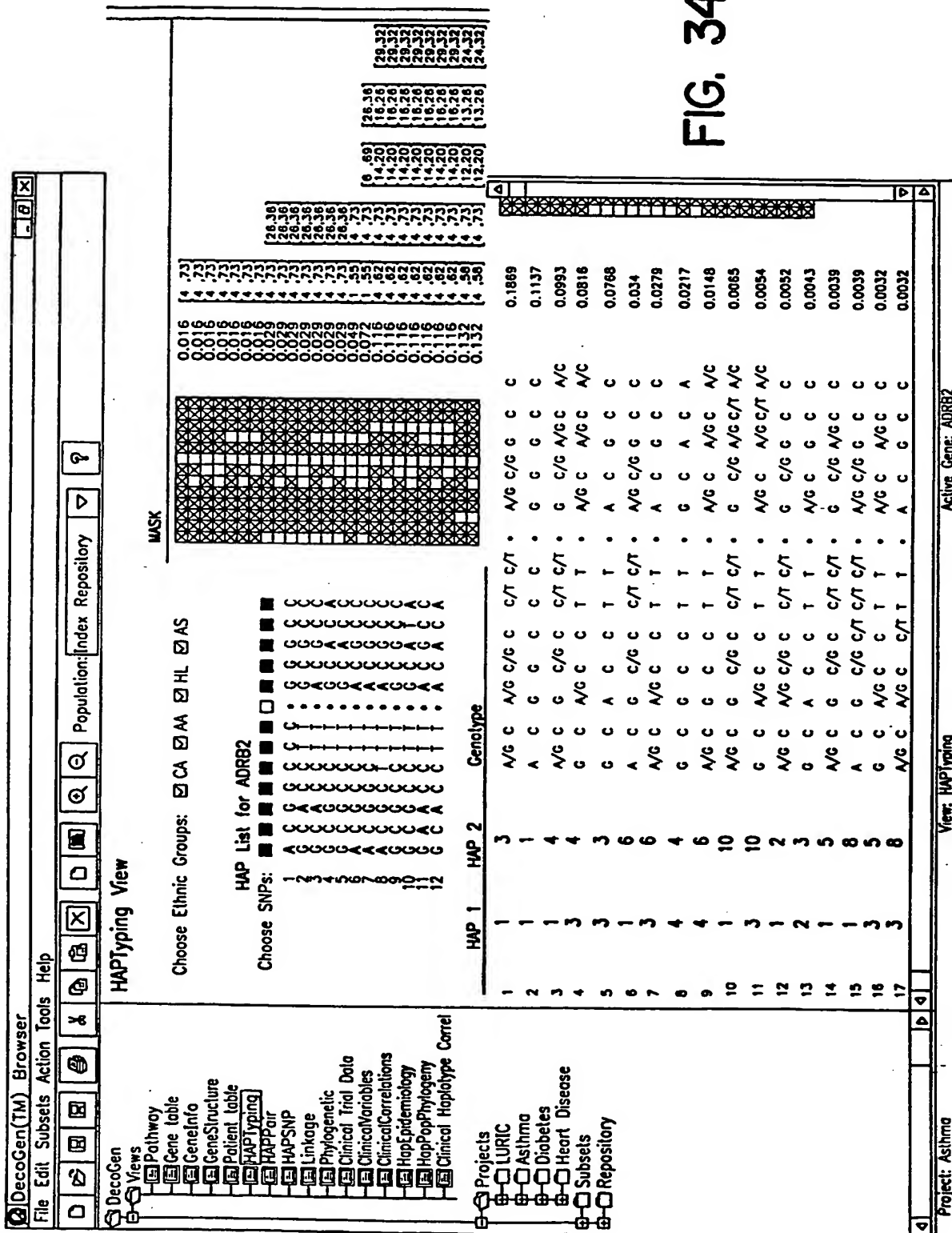
41 / 62

F/G. 33



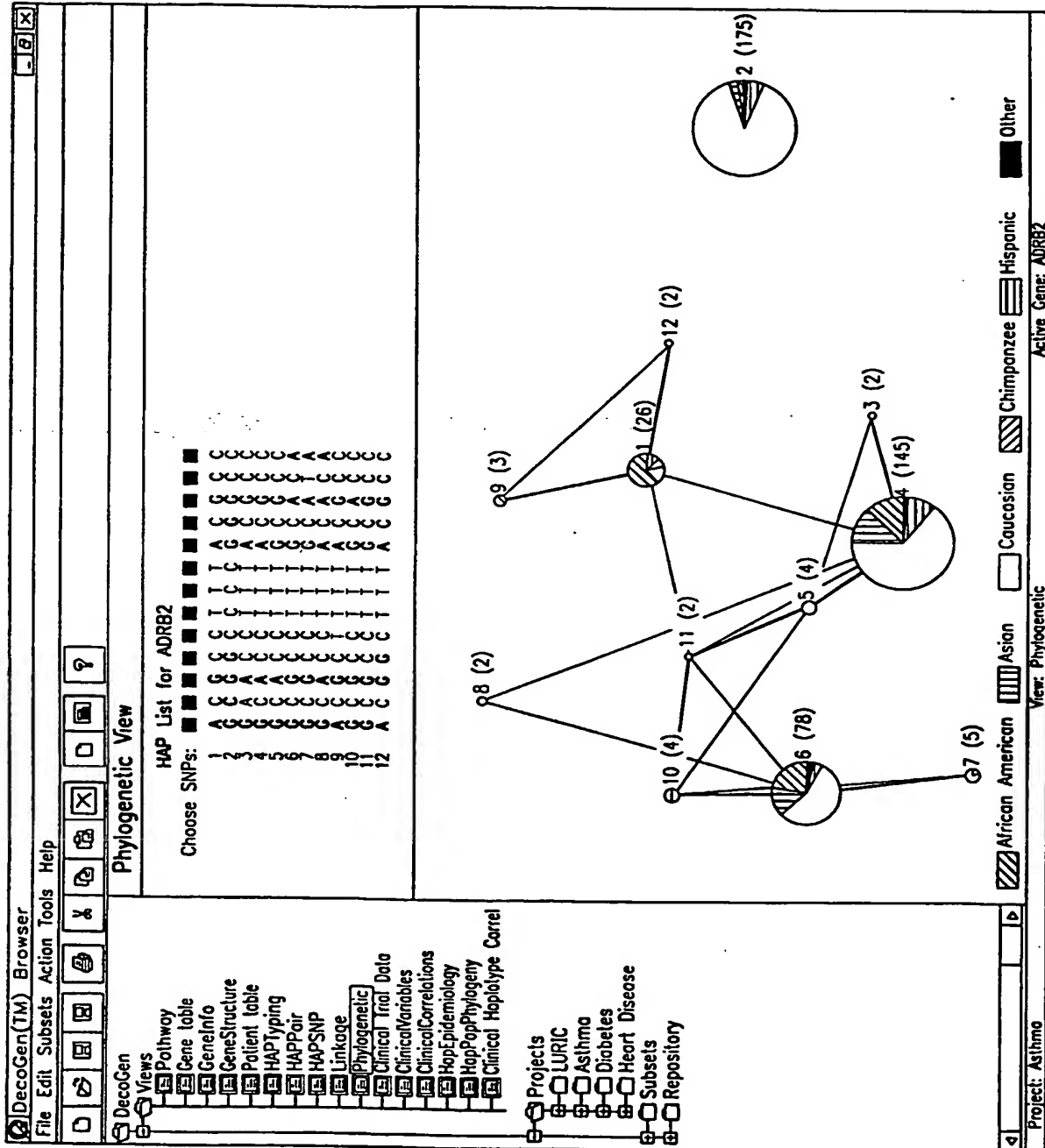
42/62

FIG. 34



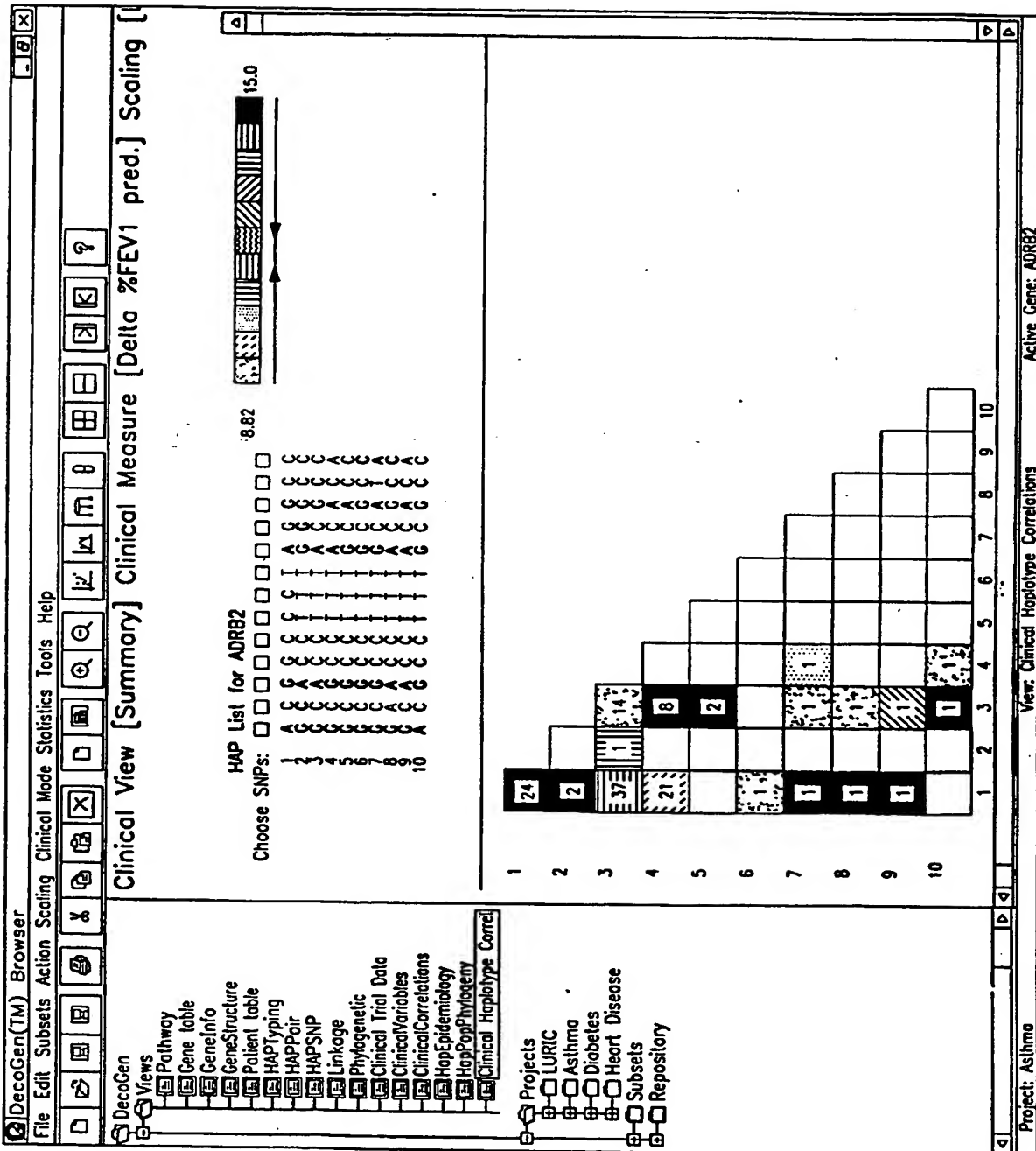
43/62

FIG. 35



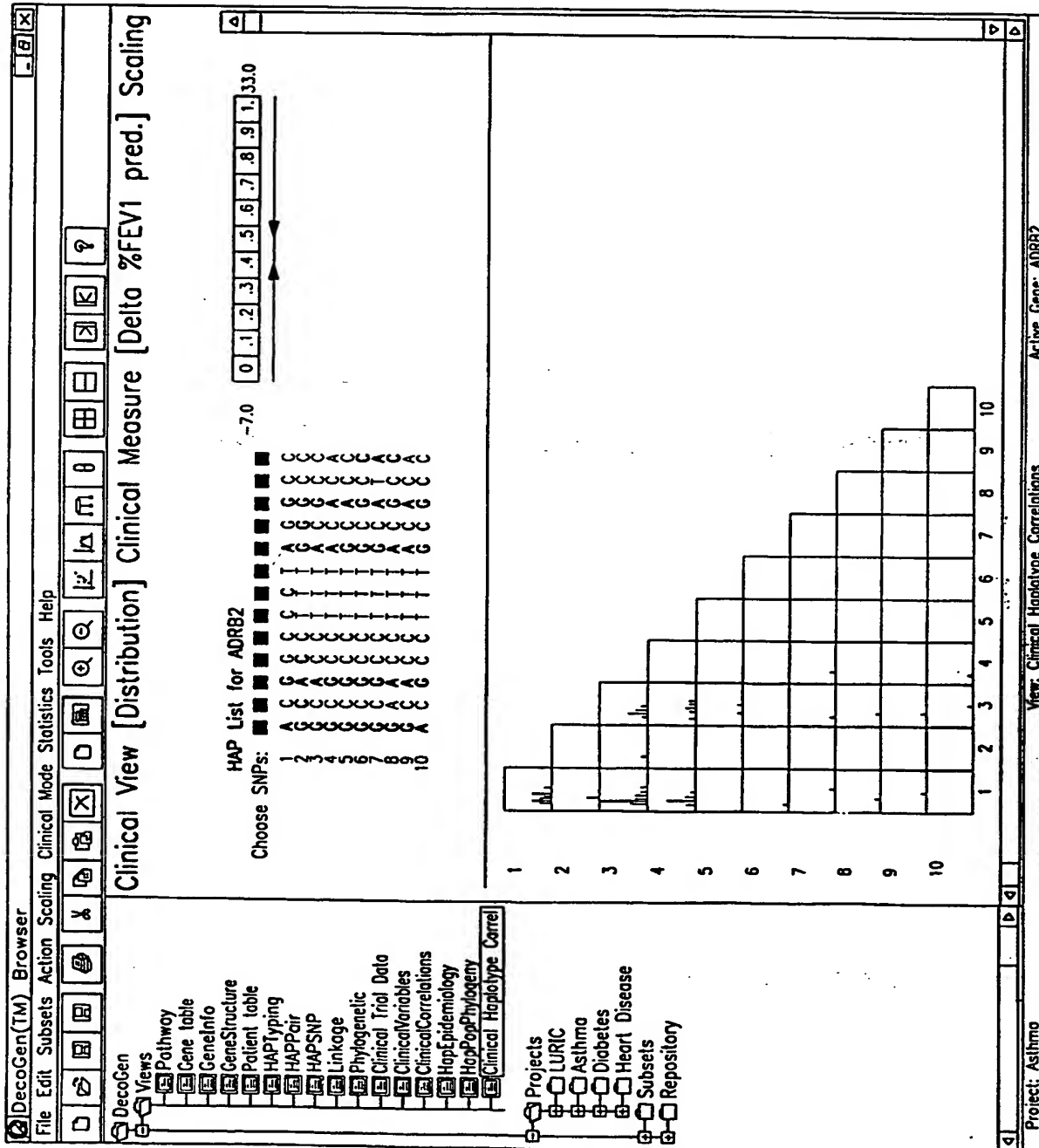
44/62

FIG. 36



45 / 62

FIG. 37



46 / 62

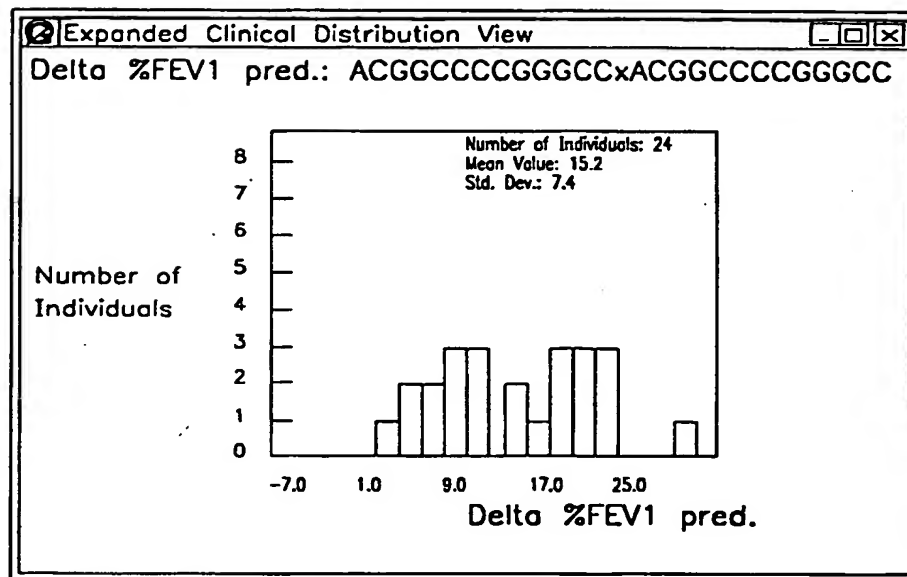


FIG. 38

47/62

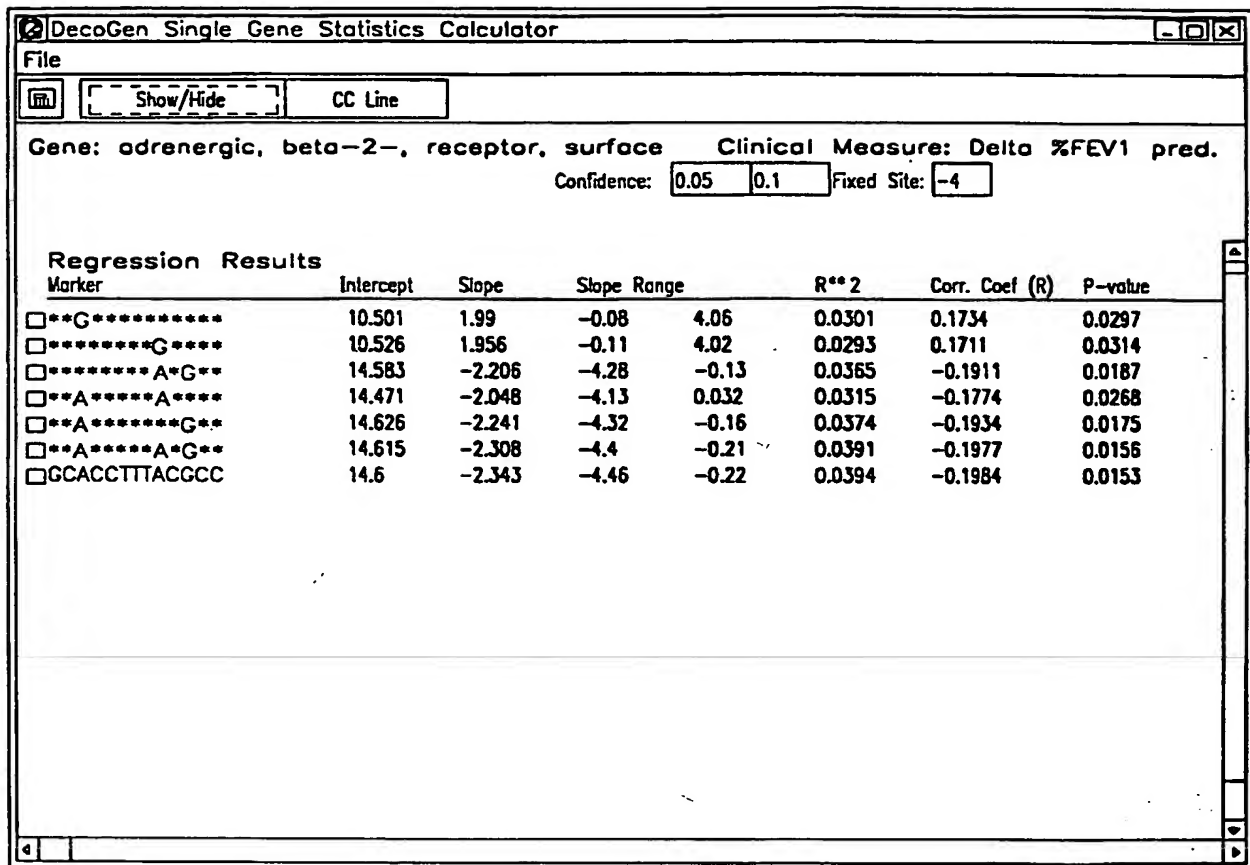


FIG. 39A

48 / 62

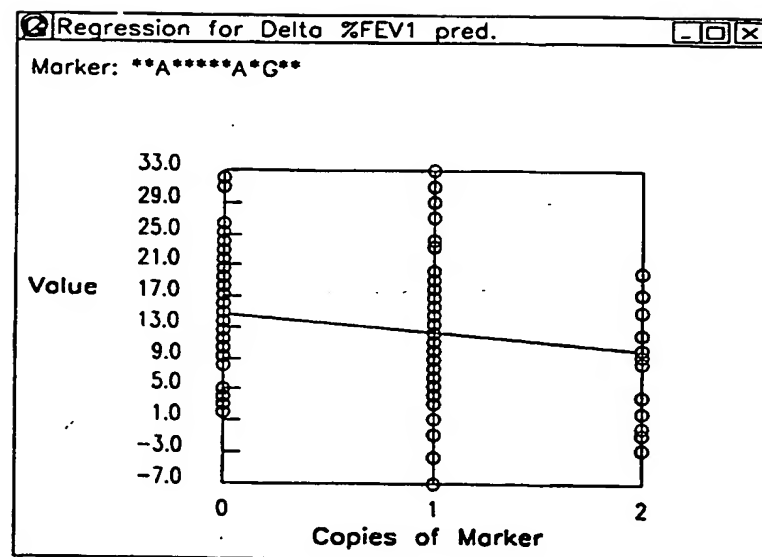
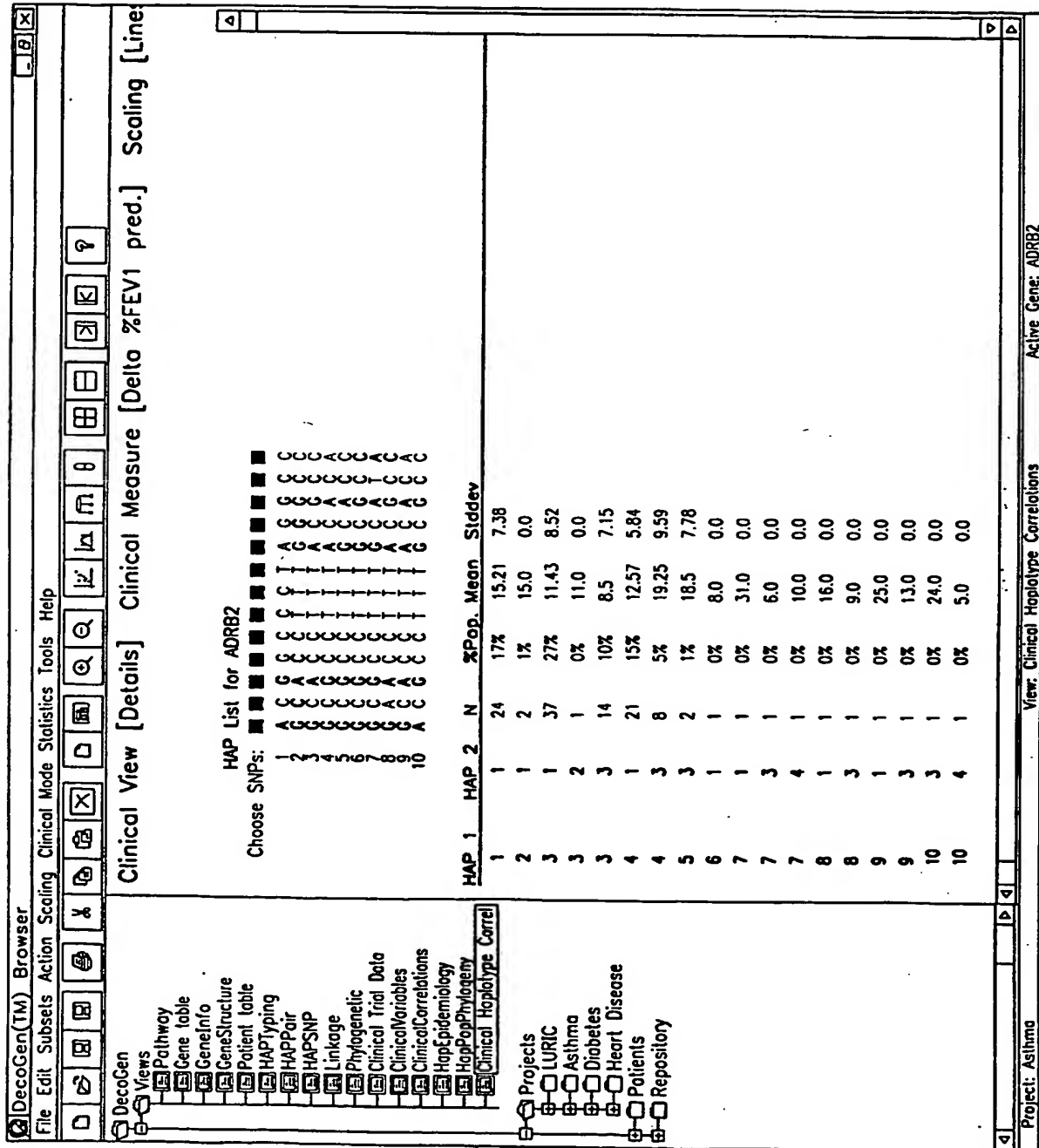


FIG. 39B

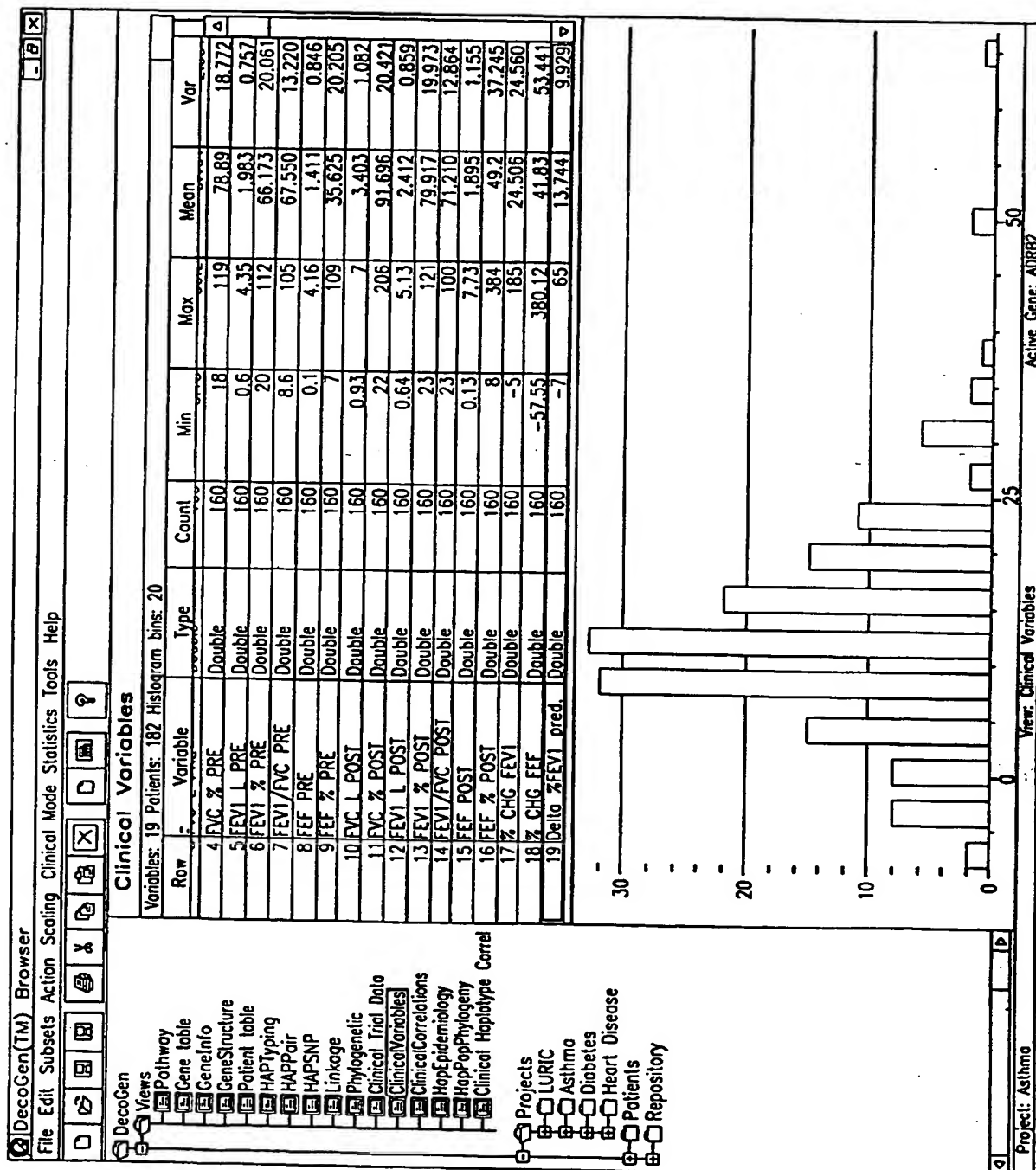
FIG. 40





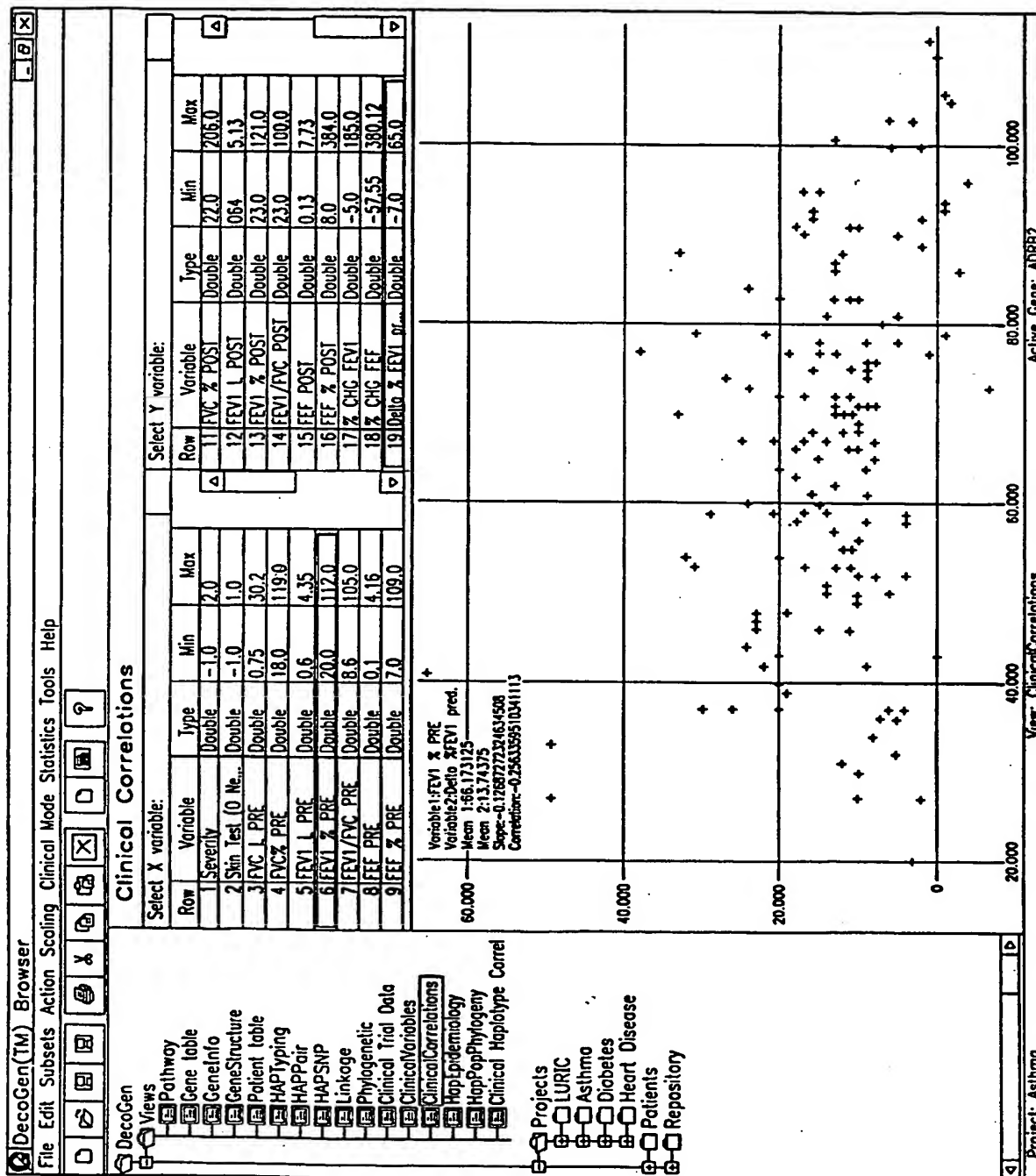
51 / 62

FIG. 42



52 / 62

FIG. 43



53 / 62

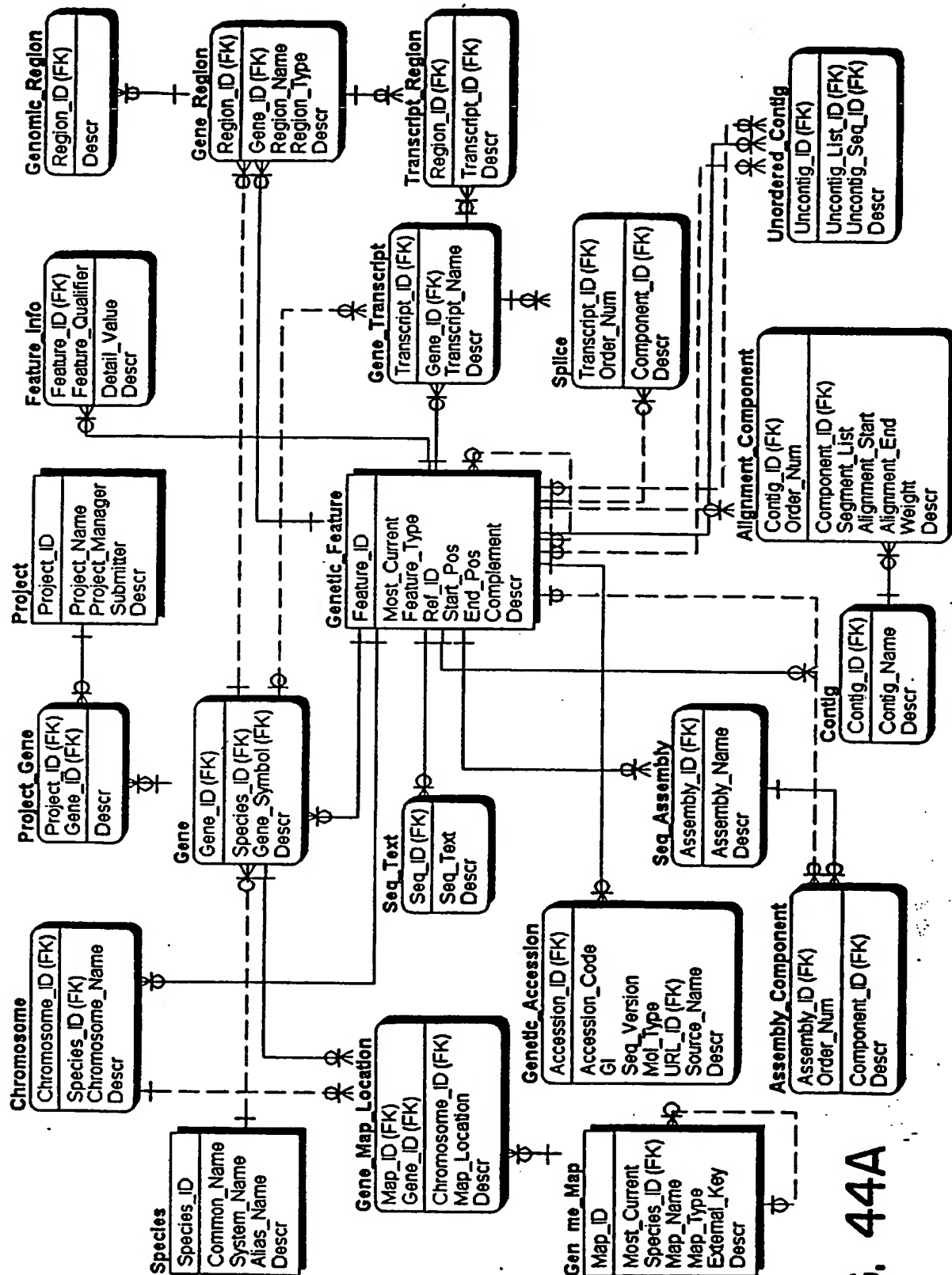


FIG. 44A

54 / 62

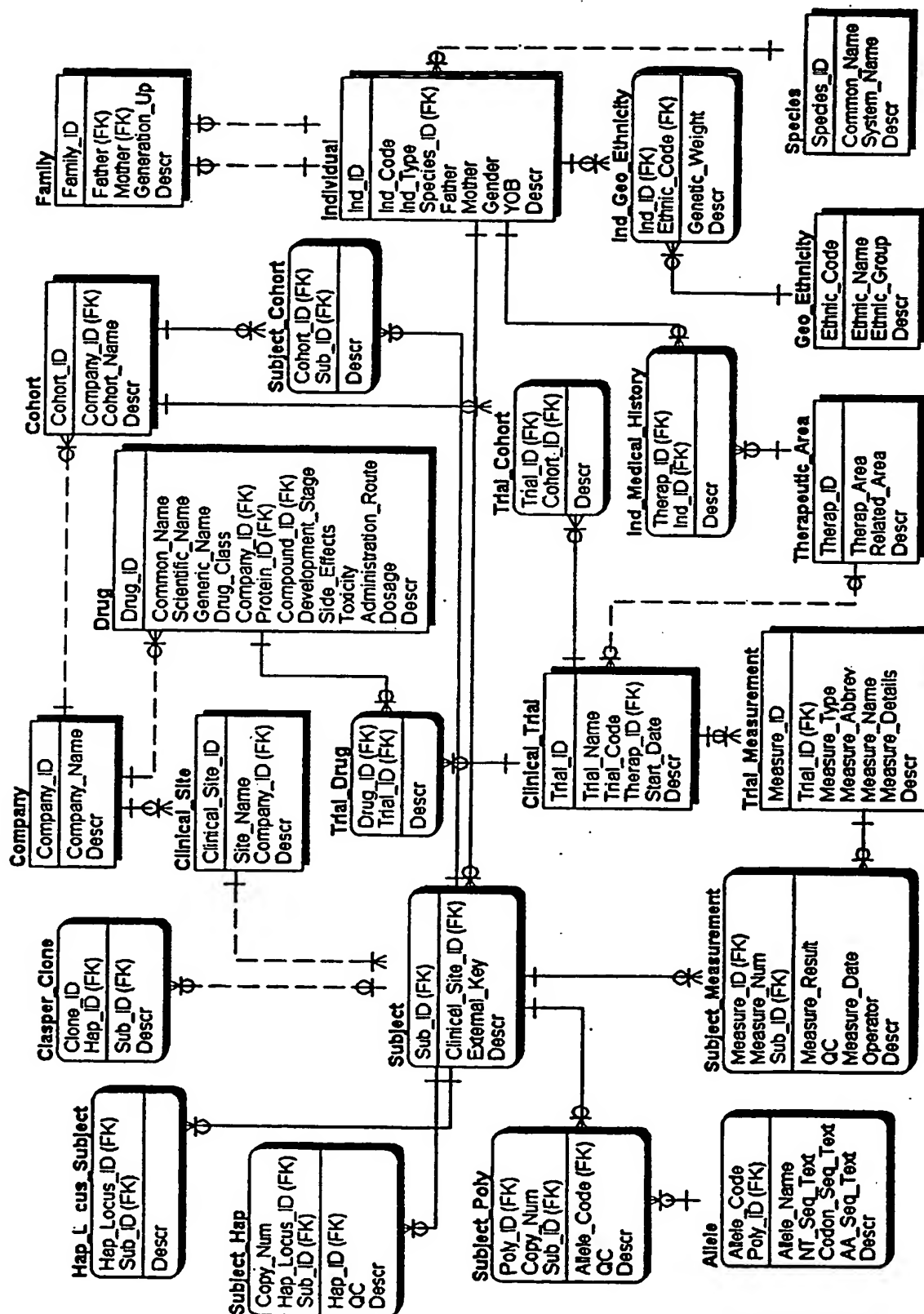


FIG. 44B

55 / 62

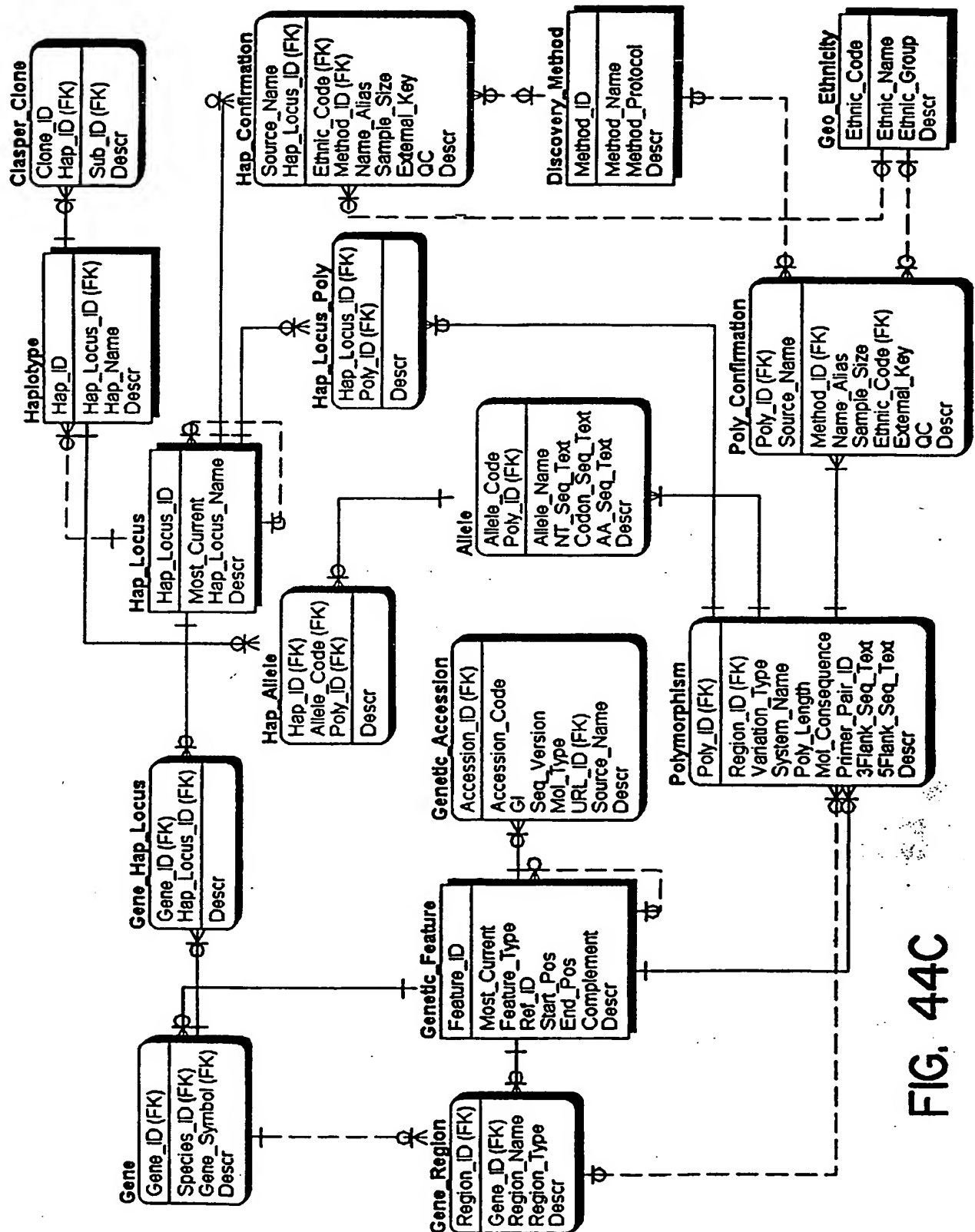


FIG. 44C

56 / 62

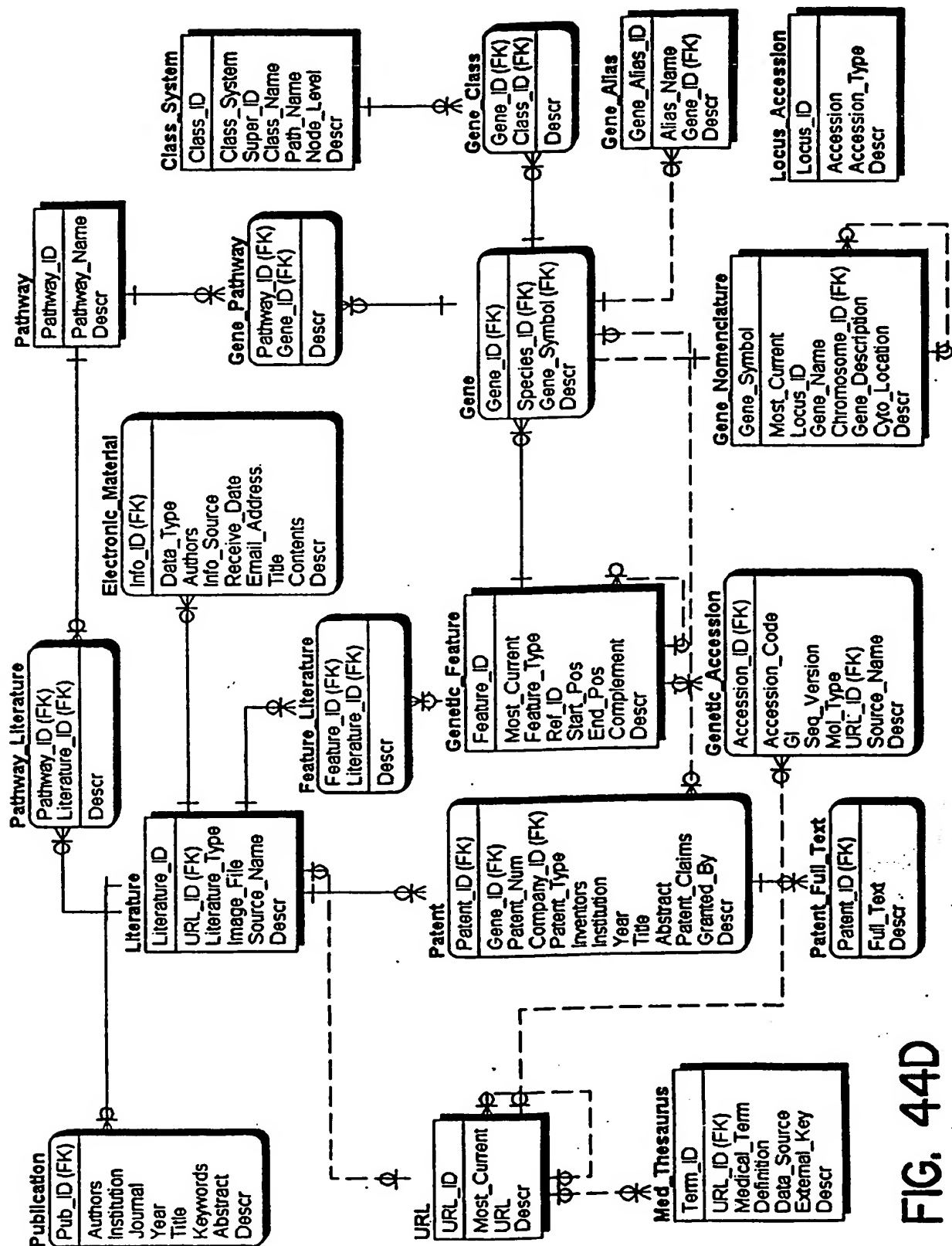


FIG. 44D

57 / 62

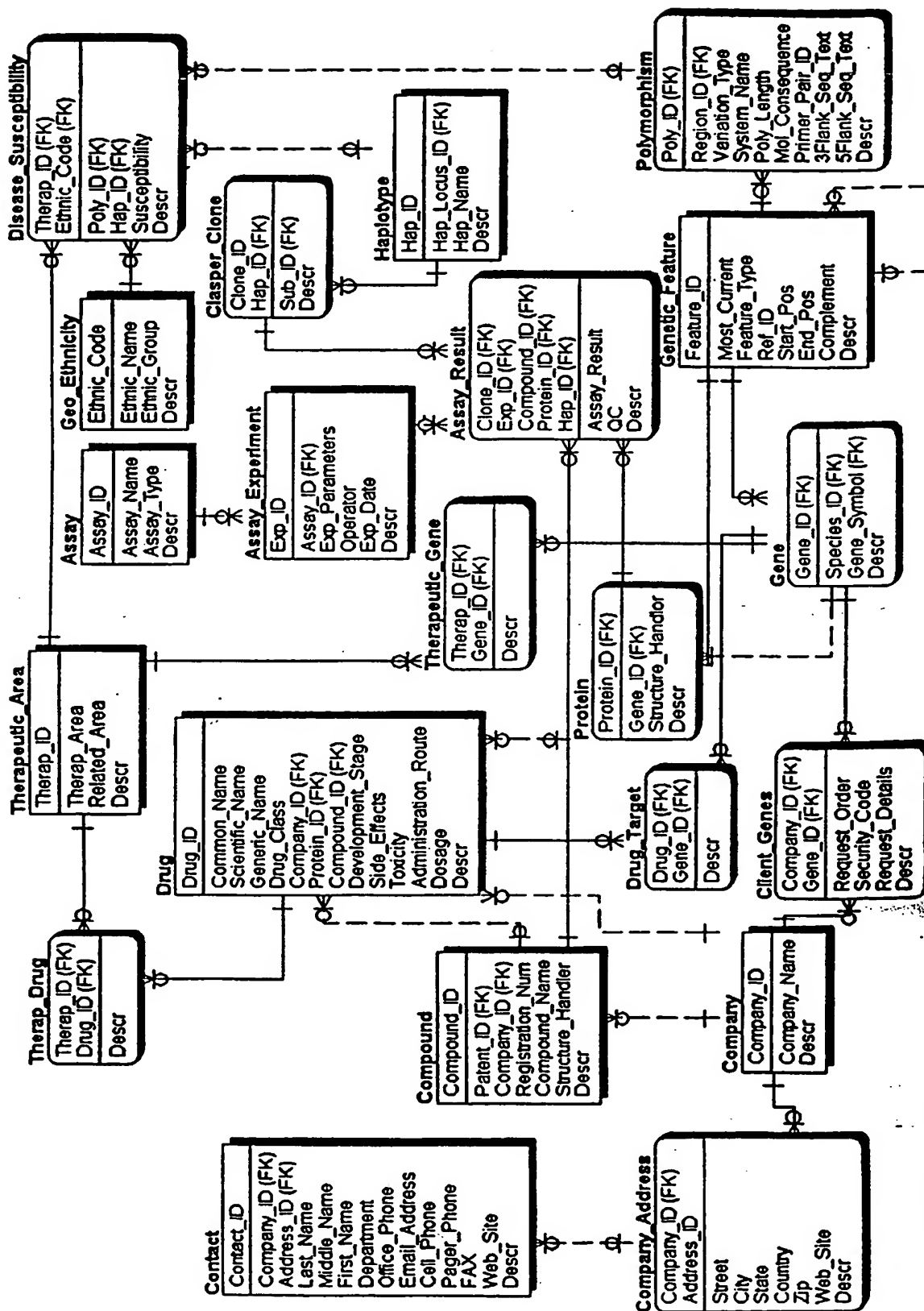
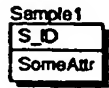


FIG. 44E

58 / 62

Legend of Figures:

Rectangle Boxes: Tables in the database.



Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 8: Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.
- 10: Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.
- 14: Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

FIG. 44F

59 / 62

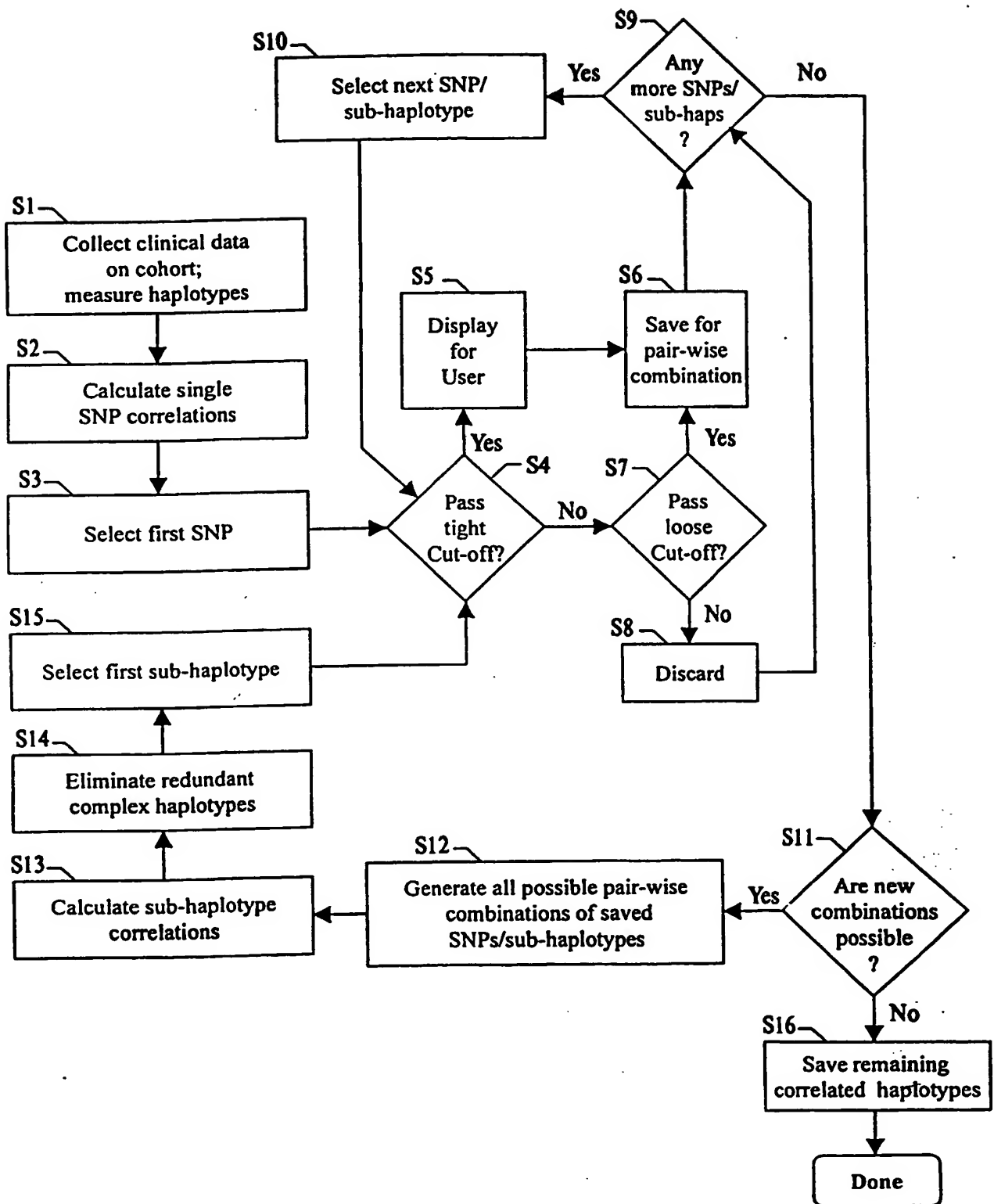


FIG. 45

SUBSTITUTE SHEET (RULE 26)

60 / 62

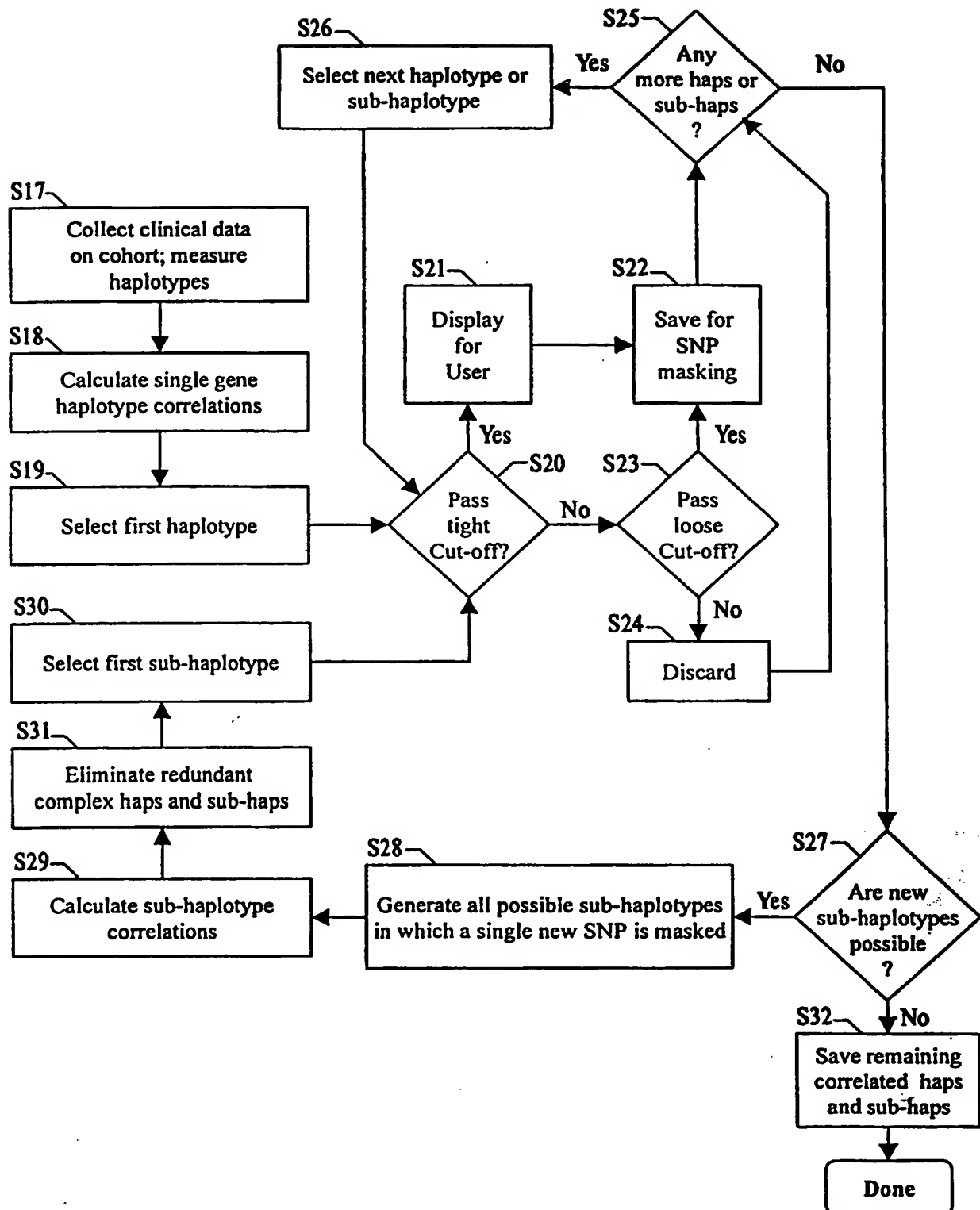


FIG. 46

61 / 62

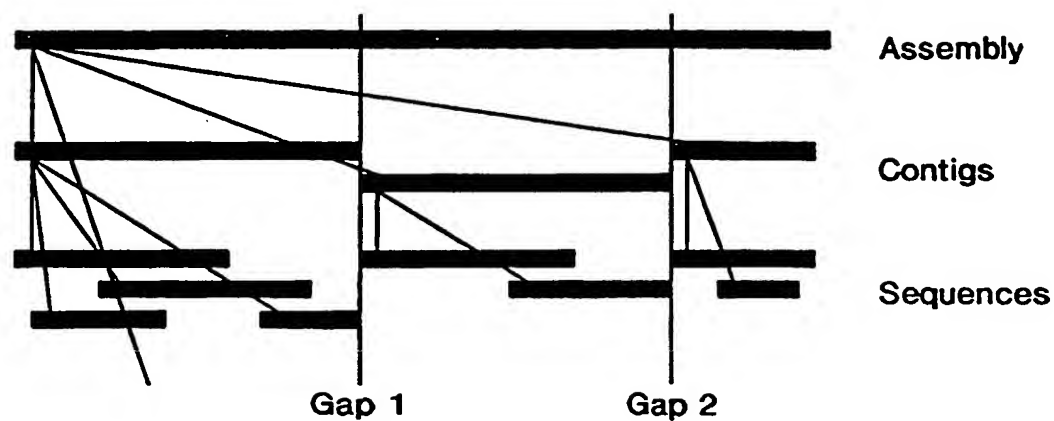


FIG. 47

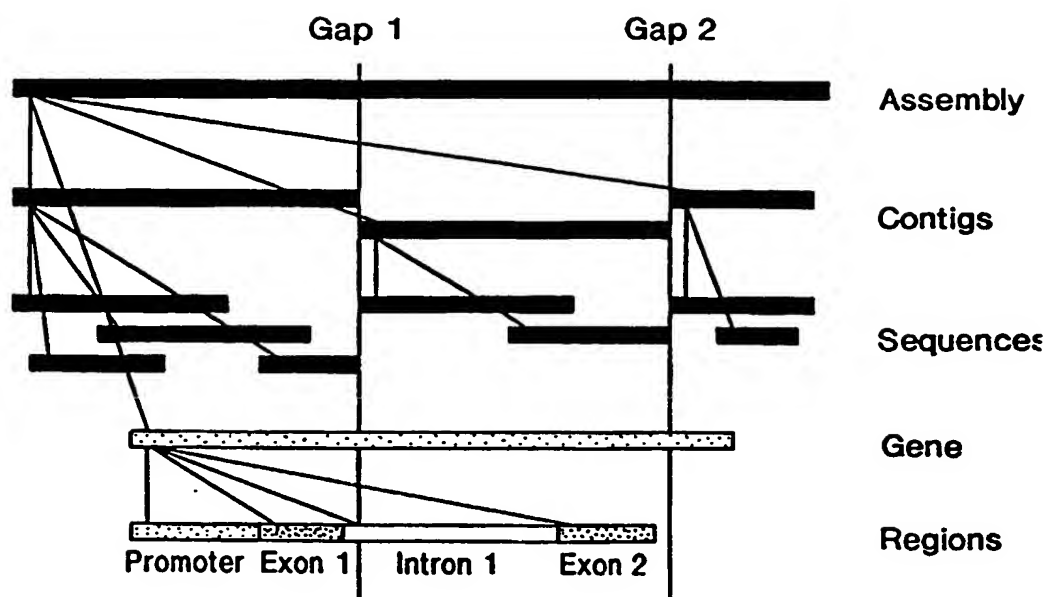


FIG. 48

62 / 62

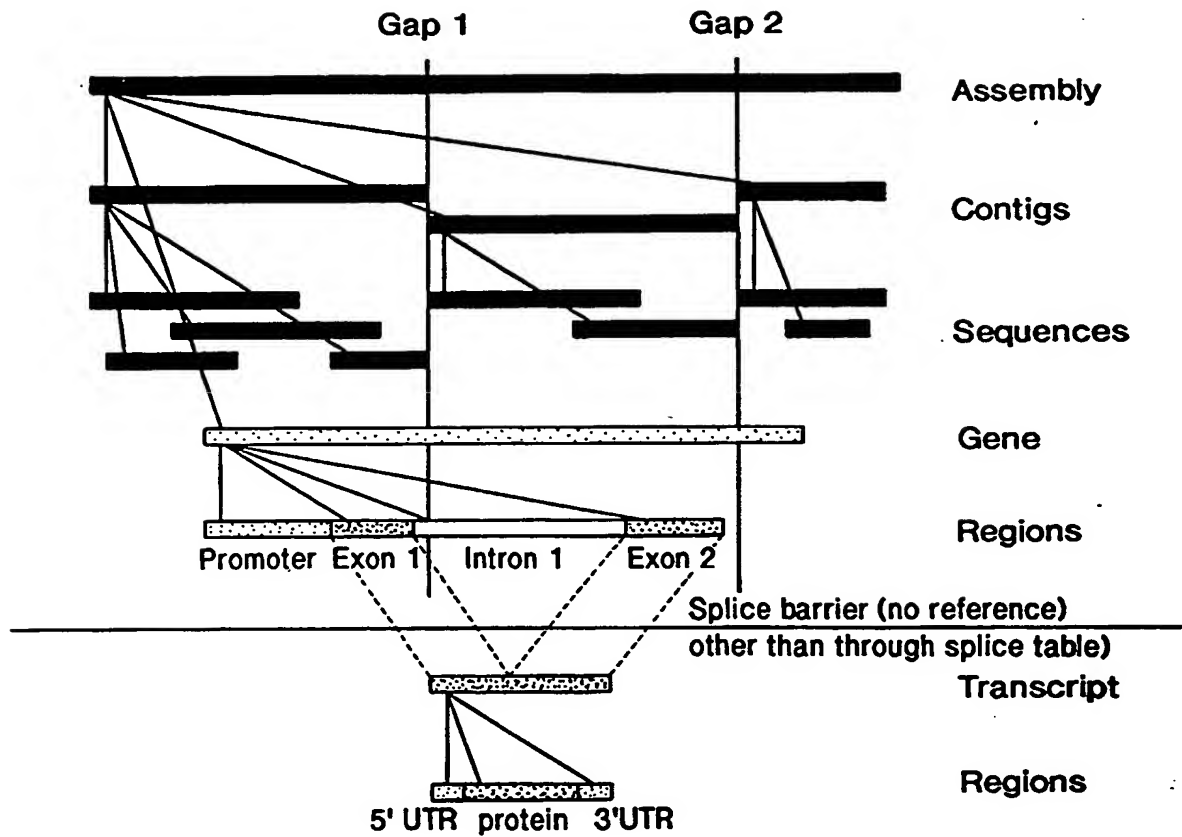


FIG. 49